

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:07:24 ; Search time 18 seconds

(without alignments)  
20.077 Million cell updates/sec

Title: US-09-854-204-2

Perfect score: 41

Sequence: 1.RRMKMKK 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 57228

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2\_6/prodata/2/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/2/1aa/backfillseq1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	41	100.0	7	4	US-09-346-847-26
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4	38	92.7	7	4	US-09-346-847-7
5	36	87.8	7	4	US-09-346-847-9
6	35	85.4	7	4	US-09-346-847-10
7	34	82.9	7	4	US-09-346-847-12
8	33	80.5	7	4	US-09-346-847-13
9	29	70.7	7	4	US-09-346-847-14
10	28	68.3	7	4	US-09-346-847-15
11	27	65.9	7	2	US-08-968-676-135
12	26	63.4	6	3	US-08-960-054A-19
13	26	63.4	6	3	US-08-958-993A-19
14	26	63.4	6	4	US-08-859-206A-8
15	26	63.4	6	4	US-09-925-715-8
16	25.5	62.2	7	4	US-09-346-847-14
17	25.5	62.2	7	4	US-09-346-847-15
18	25	61.0	6	1	US-07-841-997A-22
19	25	61.0	6	1	US-08-290-301-22
20	25	61.0	6	4	US-09-013-598-22
21	24	58.5	7	4	US-08-584-043A-95
22	23	56.1	6	1	US-07-851-941-6
23	23	56.1	6	1	US-07-851-941-7
24	23	56.1	7	1	US-08-182-175A-68
25	23	56.1	7	1	US-08-182-175A-78
26	23	56.1	7	1	US-08-474-633A-52
27	23	56.1	7	4	US-08-823-771-52

28	23	56.1	7	5	PCT-US92-06412-68	Sequence 68, Appl
29	23	56.1	7	5	PCT-US92-06412-78	Sequence 78, Appl
30	22	53.7	5	3	US-08-981-122-56	Sequence 56, Appl
31	22	53.7	6	3	US-09-260-190-3	Sequence 3, Appl
32	21	51.2	3	1	US-08-433-037-14	Sequence 14, Appl
33	21	51.2	5	1	US-07-657-769B-36	Sequence 36, Appl
34	21	51.2	5	1	US-08-165-545-5	Sequence 5, Appl
35	21	51.2	5	1	US-08-256-771-14	Sequence 14, Appl
36	21	51.2	5	1	US-07-789-184-97	Sequence 97, Appl
37	21	51.2	5	1	US-08-433-037-6	Sequence 6, Appl
38	21	51.2	5	1	US-08-475-263-97	Sequence 97, Appl
39	21	51.2	5	1	US-08-485-886-97	Sequence 97, Appl
40	21	51.2	5	1	US-08-381-984-14	Sequence 14, Appl
41	21	51.2	5	2	US-08-477-362-97	Sequence 97, Appl
42	21	51.2	5	2	US-08-477-134-97	Sequence 97, Appl
43	21	51.2	5	3	US-08-473-489A-97	Sequence 97, Appl
44	21	51.2	5	3	US-08-485-695-97	Sequence 97, Appl
45	21	51.2	5	3	US-08-981-122-27	Sequence 27, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-346-847-2
; Sequence 2, Application US/09346847
; Patent No. 6472507
; GENERAL INFORMATION:
; APPLICANT: Fischer, M. Peter
; TITLE OF INVENTION: Delivery System
; FILE REFERENCE: CCI-009
; CURRENT APPLICATION NUMBER: US/09/346,847
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: GB 9814527
; PRIOR FILING DATE: 1998-07-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-346-847-2

Query Match          100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. NO. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CQ      1 RRMKMKK 7
Db      1 RRMKMKK 7

RESULT 2
US-09-346-847-26
; Sequence 26, Application US/09346847
; Patent No. 6472507
; GENERAL INFORMATION:
; APPLICANT: Fischer, M. Peter
; TITLE OF INVENTION: Delivery System
; FILE REFERENCE: CCI-009
; CURRENT APPLICATION NUMBER: US/09/346,847
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: GB 9814527
; PRIOR FILING DATE: 1998-07-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 7
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TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (7)  
OTHER INFORMATION: AMIDATION  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-09-346-847-26

Query Match  
Best Local Similarity 100.0%; Score 41; DB 4; Length 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 1 RRMKMKK 7

RESULT 3  
US-09-346-847-6  
Sequence 6, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 6  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-346-847-6

Query Match  
Best Local Similarity 92.7%; Score 38; DB 4; Length 7;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 1 RRMKMKK 7

RESULT 4  
US-09-346-847-7  
Sequence 7, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 7  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: peptide  
US-09-346-847-7

Query Match  
Best Local Similarity 92.7%; Score 38; DB 4; Length 7;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 1 RRMKMKK 7

RESULT 5  
US-09-346-847-9  
Sequence 9, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 9  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-346-847-9

Query Match  
Best Local Similarity 87.8%; Score 36; DB 4; Length 7;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 1 RRMKMKK 7

RESULT 6  
US-09-346-847-10  
Sequence 10, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 10  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (3)  
OTHER INFORMATION: Orn  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-346-847-10

Query Match 85.4%; Score 35; DB 4; Length 7;

Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 1 RRMKMKK 7

## RESULT 7

US-09-346-847-8  
; Sequence 8, Application US/09346847  
; Patent No. 6472507  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/09/346,847  
; CURRENT FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-346-847-8

Query Match 82.3%; Score 34; DB 4; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 1 RRMKMKK 7

## RESULT 8

US-09-346-847-12  
; Sequence 12, Application US/09346847  
; Patent No. 6472507  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/09/346,847  
; CURRENT FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-346-847-12

Query Match 80.5%; Score 33; DB 4; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 1 RRMKMKK 7

## RESULT 9

US-09-346-847-13  
; Sequence 13, Application US/09346847  
; Patent No. 6472507  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/09/346,847  
; CURRENT FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (2)  
; OTHER INFORMATION: Orn  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-346-847-13

Query Match 70.7%; Score 29; DB 4; Length 7;  
Best Local Similarity 71.4%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 1 RRMKMKK 7

## RESULT 10

US-09-346-847-11  
; Sequence 11, Application US/09346847  
; Patent No. 6472507  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/09/346,847  
; CURRENT FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-346-847-11

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Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 1 RRMKMKK 7

## RESULT 11

US-08-968-676-135  
; Sequence 135, Application US/08968676

Patent No. 5919639  
GENERAL INFORMATION:  
APPLICANT: Humphreys, Robert E  
APPLICANT: Adams, Sharlene  
APPLICANT: Xu, Minzhen  
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,676  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-968-676-135

Query Match 65.9%; Score 27; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RMRKK 7  
DB 2 RMRKK 7

RESULT 12  
US-08-960-054A-19  
Sequence 19, Application US/08960054A  
Patent No. 6261537  
GENERAL INFORMATION:  
APPLICANT: Nycomed Imaging AS  
TITLE OF INVENTION: Improvements in or relating to  
TITLE OF INVENTION: diagnostic/therapeutic  
TITLE OF INVENTION: agents  
FILE REFERENCE: REF/Klaiveness/054  
CURRENT APPLICATION NUMBER: US/08/960,054A  
CURRENT FILING DATE: 1997-10-29  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 19  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial  
OTHER INFORMATION: Sequence:lipopeptide  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: Dipalmitoyl-Lys  
NAME/KEY: MOD\_RES

LOCATION: (5)  
OTHER INFORMATION: Biotinylated-Lys  
US-08-960-054A-19

Query Match 63.4%; Score 26; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KMKK 7  
DB 1 KMKK 4

RESULT 13  
US-08-958-993A-19  
Sequence 19, Application US/08958993A  
Patent No. 6264917  
GENERAL INFORMATION:  
APPLICANT: Nycomed Imaging AS  
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic  
TITLE OF INVENTION: agents  
FILE REFERENCE: REF/Klaiveness/993  
CURRENT APPLICATION NUMBER: US/08/958,993A  
CURRENT FILING DATE: 1997-10-28  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 19  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:lipopeptide  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: Dipalmitoyl-Lys  
NAME/KEY: MOD\_RES  
LOCATION: (5)  
OTHER INFORMATION: Biotinylated-Lys  
US-08-958-993A-19

Query Match 63.4%; Score 26; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KMKK 7  
DB 1 KMKK 4

RESULT 14  
US-08-959-206A-8  
Sequence 8, Application US/08959206A  
Patent No. 6331289  
GENERAL INFORMATION:  
APPLICANT: Nycomed Imaging AS  
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic  
TITLE OF INVENTION: agents  
FILE REFERENCE: REF/Klaiveness/206  
CURRENT APPLICATION NUMBER: US/08/959,206A  
CURRENT FILING DATE: 1997-10-24  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 8  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:lipopeptide  
NAME/KEY: MOD\_RES  
LOCATION: (5)  
OTHER INFORMATION: Biotinylated-Lys  
NAME/KEY: MOD\_RES  
LOCATION: (1)

OTHER INFORMATION: Dipalmitoyl-lysine  
US-08-959-206A-8

Query Match 63.4%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KWKK 7  
DB 1 KWKK 4

RESULT 15  
US-09-925-715-8  
; Sequence 8, Application US/09925715  
; Patent No. 668047  
; GENERAL INFORMATION:  
; APPLICANT: Mycomed Imaging AS  
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic  
; FILE REFERENCE: REF/Klavness/206  
; CURRENT APPLICATION NUMBER: US/09/925,715  
; CURRENT FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:lipopeptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: Biotinylated-Lys  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Dipalmitoyl-lysine  
US-09-925-715-8

Query Match 63.4%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KWKK 7  
DB 1 KWKK 4

Search completed: August 11, 2004, 14:10:27  
Job time : 19 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2004, 13:58:42 ; Search time 16 seconds  
(without alignments)  
42.084 Million cell updates/sec

Title: US-09-854-204-2  
Perfect score: 41  
Sequence: 1 RRMKWK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	33	2	SS7235
2	41	100.0	42	2	I65241
3	41	100.0	42	2	I65249
4	41	100.0	45	2	PC1216
5	41	100.0	48	2	I51439
6	41	100.0	60	2	PC2399
7	41	100.0	60	2	PC2400
8	41	100.0	60	2	S93227
9	41	100.0	60	2	I51437
10	41	100.0	62	2	B12391
11	41	100.0	66	2	S15536
12	41	100.0	66	2	S15538
13	41	100.0	66	2	S15534
14	41	100.0	67	2	B27471
15	41	100.0	69	2	S13785
16	41	100.0	70	2	B37042
17	41	100.0	71	2	UC1161
18	41	100.0	71	2	A60084
19	41	100.0	74	2	D34510
20	41	100.0	75	2	I51341
21	41	100.0	75	2	S58852
22	41	100.0	76	2	C43559
23	41	100.0	78	2	I51342
24	41	100.0	81	2	S47605
25	41	100.0	81	2	B29585
26	41	100.0	81	2	A25180
27	41	100.0	82	2	S08302
28	41	100.0	83	2	S47603
29	41	100.0	83	2	S50066

30	41	100.0	85	2	I65198	homeotic protein H
31	41	100.0	85	2	A25472	homeotic protein H
32	41	100.0	86	2	A34510	homeotic protein H
33	41	100.0	86	2	UT0489	homeotic protein Z
34	41	100.0	86	2	S08303	homeotic protein H
35	41	100.0	87	2	S00589	homeotic protein H
36	41	100.0	88	2	A03317	homeotic protein M
37	41	100.0	95	2	B22830	homeotic protein H
38	41	100.0	96	2	S08639	homeotic protein Z
39	41	100.0	96	2	A05266	homeotic protein H
40	41	100.0	96	2	A55278	homeotic protein H
41	41	100.0	97	2	C27176	homeotic protein H
42	41	100.0	97	2	A24779	homeotic protein m
43	41	100.0	99	2	A41605	homeotic protein H
44	41	100.0	103	2	A32167	homeotic protein H
45	41	100.0	104	2	D43559	homeotic protein H

## ALIGNMENTS

RESULT 1  
S57235  
antennapedia protein (clone p1105) - fruit fly (Drosophila pseudoobscura) (fragment)  
C/Species: Drosophila pseudoobscura  
C/Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 15-Oct-1999  
C/Accession: S57235  
R/Randazzo, F.M.; Seeger, M.A.; Huss, C.A.; Sweeney, M.A.; Cecil, J.K.; Kaufman, T.C.  
Genetics 133, 319-330, 1993  
A/Title: Structural changes in the antennapedia complex of Drosophila pseudoobscura.  
A/Reference number: S57224  
A/Accession: S57235  
A/Molecule type: DNA  
A/Residues: 1-33 <RAN>  
A/Cross-References: EMBL:X77711  
C/Genetics:  
A/Gene: FlyBase:Antp  
A/Cross-References: FlyBase:FBgn0012693  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F/1-22/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 41; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.36; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;  
QY 1 RRMKWK 7  
DB 16 RRMKWK 22

RESULT 2  
I65241  
homeotic protein Hox-A - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 15-Oct-1999  
C/Accession: I65241  
R/Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.  
Biochem. Genet. 32, 351-360, 1994  
A/Title: Cloning of rat homeobox genes.  
A/Reference number: I52340; MUID:95217128; PMID:7702549  
A/Accession: I65241  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-42 <RSS>  
A/Cross-References: GB:S76290; NID:913077  
C/Genetics:  
A/Gene: Hox-A; Hox-1  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F/1-40/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 41; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRMKMKK 7  
Db 34 RRMKMKK 40

RESULT 3  
165249  
homeoprotein 13A - rat (fragment)  
C/Species: Rattus sp. (rat)  
C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 05-Nov-1999  
C/Accession: 165249  
R/Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.  
Biochem. Genet. 32, 351-360, 1994  
A/Title: Cloning of rat homeobox genes.  
A/Reference number: 152340; PMID:95217128; PMID:7702549  
A/Accession: 165249  
A/Status: Preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-42 <RES>  
A/Cross-references: GB:S76307; NID:9913074; PIDN:AA33921.1; PID:9913075

Query Match  
Best Local Similarity 100.0%; Score 41; DB 2; Length 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 34 RRMKMKK 40

RESULT 4  
PC1216  
homeotic protein Dthb1 - planarian (Dugesia tigrina) (fragment)  
C/Species: Dugesia tigrina  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Oct-1997  
C/Accession: PC1216  
R/Oliver, G.; Vispo, M.; Malinos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlich  
Gene 121, 337-342, 1992  
A/Title: Homeoboxes in flatworms.  
A/Reference number: JCI386; PMID:93077050; PMID:1359988  
A/Accession: PC1216  
A/Molecule type: DNA  
A/Residues: 1-45 <OLIT>  
A/Cross-references: EMBL:X66822  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
P/1-45/Domain: homeobox homology (fragment) <HOX>

Query Match  
Best Local Similarity 100.0%; Score 41; DB 2; Length 45;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 39 RRMKMKK 45

RESULT 5  
151439  
homeobox protein - African clawed frog (fragment)  
C/Species: Xenopus laevis (African clawed frog)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 15-Oct-1999  
C/Accession: 151439  
R/LeRoy, P.; DeRobertis, E.M.  
Dev. Dyn. 194, 21-32, 1992  
A/Title: Effects of lithium chloride and retinoic acid on the expression of genes from  
A/Reference number: 151439; PMID:93043517; PMID:1384809  
A/Accession: 151439  
A/Status: Preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA

A/Residues: 1-48 <LER>  
A/Cross-references: GB:M91587; NID:9214257; PIDN:AAA49750.1; PID:9214258  
C/Genetics:  
A/Gene: Hox2.2  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
P/1-27/Domain: homeobox homology (fragment) <HOX>

Query Match  
Best Local Similarity 100.0%; Score 41; DB 2; Length 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 21 RRMKMKK 27

RESULT 6  
PC2399  
antennapedia-like homeotic protein ABox 2 - sea squirt (Styela clava) (fragment)  
C/Species: Styela clava  
C/Date: 13-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 21-Jul-2000  
C/Accession: PC2399  
R/Ge, T.; Lee, H.; Tomlinson, C.R.  
Gene 147, 219-222, 1994  
A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela  
A/Reference number: PC2399; PMID:95011617; PMID:7926803  
A/Accession: PC2399  
A/Molecule type: DNA  
A/Residues: 1-60 <GET>  
A/Cross-references: GB:S73920; NID:9653714; PIDN:AA33061.2; PID:97387472  
A/Note: The authors translated the codon ATT for residue 47 as Glu  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
P/2-58/Domain: homeobox homology <HOX>

Query Match  
Best Local Similarity 100.0%; Score 41; DB 2; Length 60;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 52 RRMKMKK 58

RESULT 7  
PC2400  
antennapedia-like homeotic protein AHox 3 - sea squirt (Styela plicata) (fragment)  
C/Species: Styela plicata  
C/Date: 26-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 17-Oct-1997  
C/Accession: PC2400  
R/Ge, T.; Lee, H.; Tomlinson, C.R.  
Gene 147, 219-222, 1994  
A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela  
A/Reference number: PC2399; PMID:95011617; PMID:7926803  
A/Accession: PC2400  
A/Molecule type: DNA  
A/Residues: 1-60 <GET>  
A/Note: The authors translated the codon ATA for residue 47 as Glu  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
P/2-58/Domain: homeobox homology <HOX>

Query Match  
Best Local Similarity 100.0%; Score 41; DB 2; Length 60;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
Db 52 RRMKMKK 58

RESULT 8



S09227  
 homeotic protein Htr-A2 - leech (*Helobdella triseriatis*) (fragment)  
 C:Species: *Helobdella triseriatis*  
 C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 24-Sep-1999  
 C:Accession: S09227  
 R:Medeen, C.U.; Kosteriken, R.G.; Matsumura, I.; Weisblat, D.A.  
 Nucleic Acids Res. 18, 1908, 1990  
 A:Title: Evidence for a new family of evolutionarily conserved homeobox genes.  
 A:Reference number: S09227; MUID:90245602; PMID:1570867  
 A:Accession: S09227  
 A:Molecule type: DNA  
 A:Residues: 1-60 <MED>  
 A:Cross-references: EMBL:X51752; NID:g9463; PIND:CAA3604.1; PID:g20267; PID:g1335706  
 A>Note: the authors translated the codon TTC for residue 14 as Leu  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 0.66; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 52 RRMKMKK 58

RESULT 9  
 151437  
 homeotic protein Hox 2.4 - African clawed frog (fragment)  
 C:Species: *Xenopus laevis* (African clawed frog)  
 C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 24-Sep-1999  
 C:Accession: 151437  
 R:Bitner, D.  
 Dev. Dyn. 196, 11-24, 1993  
 A:Title: Characterization of the *Xenopus* Hox 2.4 gene and identification of control element  
 A:Reference number: 151437; MUID:93326800; PMID:7916675  
 A:Accession: 151437  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-60 <BIT>  
 A:Cross-references: GB:M83947; NID:g214252; PIND:AAA49748.1; PID:g214253  
 C:Genetics:  
 A:Gene: Hox 2.4  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 0.66; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 52 RRMKMKK 58

RESULT 10  
 B32391  
 homeotic protein Hox 2.4 - mouse  
 C:Species: *Mus musculus* (house mouse)  
 C>Date: 08-Dec-1989 #sequence\_revision 08-Dec-1989 #text\_change 17-Oct-1997  
 C:Accession: B32391  
 R:Graham, A.; Papalopulu, N.; Krumlauf, R.  
 Cell 57, 367-378, 1989  
 A:Title: The murine and *Drosophila* homeobox gene complexes have common features of organ  
 A:Reference number: A32391; MUID:85249299; PMID:2566383  
 A:Accession: B32391  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: DNA  
 A:Residues: 1-62 <GRA>  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 0.68; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 52 RRMKMKK 58

RESULT 11  
 S15536  
 homeotic protein Hox A7 - human (fragment)  
 N:Alternate names: homeotic protein Hox 1A  
 C:Species: *Homo sapiens* (man)  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 29-Aug-1997  
 C:Accession: S15536  
 R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc  
 Genome 31, 745-756, 1989  
 A:Title: Organization of human Class I homeobox genes.  
 A:Reference number: S15036; MUID:90215256; PMID:2576652  
 A:Accession: S15536  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-66 <BN>  
 C:Genetics:  
 A:Gene: GDB:HOXA7  
 A:Cross-references: GDB:120647; OMIM:142950  
 A:Map position: 7p15.3-7p15.3  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 0.72; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 52 RRMKMKK 58

RESULT 12  
 S15538  
 homeotic protein Hox A6 - human (fragment)  
 N:Alternate names: homeotic protein Hox 1B  
 C:Species: *Homo sapiens* (man)  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 29-Aug-1997  
 C:Accession: S15538  
 R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc  
 Genome 31, 745-756, 1989  
 A:Title: Organization of human Class I homeobox genes.  
 A:Reference number: S15036; MUID:90215256; PMID:2576652  
 A:Accession: S15538  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-66 <BN>  
 C:Genetics:  
 A:Gene: GDB:HOXA6  
 A:Cross-references: GDB:120648; OMIM:142951  
 A:Map position: 7p15.3-7p15.3  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 0.72; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 52 RRMKMKK 58

## RESULT 13

S15534  
 homeotic protein Hox C8 - human (fragment)  
 N:Alternate names: homeotic protein Hox 3A  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 29-Aug-1997  
 C/Accession: S15534  
 R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc  
 Genome 31, 745-756, 1989  
 A>Title: Organization of human class I homeobox genes.  
 A:Reference number: S15036; MUID:90215256; PMID:2576652  
 A/Accession: S15534  
 A>Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-66 <BON>  
 C:Genetics:  
 A:Gene: GDB:HOXC8  
 A:Cross-references: GDB:120668; OMIM:142970  
 A:Map position: 12q13.3-12q13.3  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 0.72;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
 |||||  
 Db 52 RRMKKKK 58

## RESULT 14

B27471  
 homeotic protein R2 - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 17-Nov-2000  
 C/Accession: B27471; 165243  
 R:Palzon, M.; Sanderson, N.; Chung, S.Y.  
 Gene 54, 23-32, 1987  
 A>Title: Cloning and expression of rat homeo-box-containing sequences.  
 A:Reference number: A91576; MUID:87277429; PMID:2886401  
 A/Accession: B27471  
 A:Molecule type: DNA  
 A:Residues: 1-67 <FAL>  
 R:Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.  
 Biochem. Genet. 32, 351-360, 1994  
 A>Title: Cloning of rat homeobox genes.  
 A:Reference number: 152340; MUID:95217128; PMID:7702549  
 A/Accession: 165243  
 A>Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-42 <RES>  
 A:Cross-references: GB:S76296; NID:913079  
 C:Genetics:  
 A:Gene: Hox-A; Hox-1  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:1-40/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 41; DB 2; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 0.73;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
 |||||  
 Db 34 RRMKKKK 40

## RESULT 15

S13785

homeotic protein m31 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 19-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 17-Oct-1997  
 C/Accession: S13785  
 R:Breiter, G.; Bucan, M.; Francke, U.; Colberg-Poley, A.M.; Gruss, P.  
 EMBO J. 5, 2209-2215, 1986  
 A>Title: Sequential expression of murine homeo box genes during F9 EC cell differentiation  
 A:Reference number: S13785; MUID:87053860; PMID:2877873  
 A/Accession: S13785  
 A:Molecule type: DNA  
 A:Residues: 1-69 <BR3>  
 C:Genetics:  
 A:Map position: 15  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 0.75;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
 |||||  
 Db 52 RRMKKKK 58

Search completed: August 11, 2004, 14:02:15  
 Job time : 16 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2004, 13:54:57 ; Search time 13 Seconds  
(without alignments)

28.038 Million cell updates/sec

Title: US-09-854-204-2

Perfect score: 41

Sequence: 1 RRMKWK 7

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	48	1 HXB6_XENLA	P31256 xenopus lae
2	41	100.0	49	1 HXA5_SHEEP	Q28599 ovis aries
3	41	100.0	60	1 HMA2_HELTR	P17138 heliodella
4	41	100.0	67	1 HXA4_RAT	P09635 rattus norv
5	41	100.0	71	1 HXA7_SHEEP	Q28600 ovis aries
6	41	100.0	71	1 HXC5_NOTVI	P31262 notonitum
7	41	100.0	74	1 HMG9_APIME	P15660 apis mellif
8	41	100.0	75	1 HMSA_SALSA	P09636 salmo salar
9	41	100.0	76	1 HXC4_RAT	P18665 rattus norv
10	41	100.0	78	1 HXA5_SALSA	P09637 salmo salar
11	41	100.0	80	1 HXA4_LINSA	P81192 linus sang
12	41	100.0	81	1 HXS1_BRARE	P09013 brachydanio
13	41	100.0	82	1 HXB5_CHICK	P14538 gallus gall
14	41	100.0	84	1 HXB6_CHICK	P14539 gallus gall
15	41	100.0	86	1 SCR_APIME	P15659 apis mellif
16	41	100.0	87	1 HXA4_SHEEP	Q28598 ovis aries
17	41	100.0	87	1 HXC5_XENLA	P09020 xenopus lae
18	41	100.0	92	1 HXB8_RAT	P18663 rattus norv
19	41	100.0	93	1 HXB8_PIG	P09078 sus scrofa
20	41	100.0	96	1 HXC6_BRARE	P15662 brachydanio
21	41	100.0	105	1 HXA7_RAT	P09634 rattus norv
22	41	100.0	105	1 HXB4_BRARE	P22574 brachydanio
23	41	100.0	108	1 HXC8_RAT	P18666 rattus norv
24	41	100.0	112	1 HXB7_RAT	P18664 rattus norv
25	41	100.0	133	1 BRX2_SHEEP	Q90002 ovis aries
26	41	100.0	148	1 HXA5_HUMAN	P50208 ambystoma m
27	41	100.0	153	1 HXC6_SHEEP	P49925 ovis aries
28	41	100.0	188	1 HXD8_CHICK	P23459 gallus gall
29	41	100.0	207	1 BRX1_CHICK	Q96688 gallus gall
30	41	100.0	208	1 HXA7_HETR	Q91a25 heterodontu
31	41	100.0	209	1 HXA7_XENLA	P09071 xenopus lae
32	41	100.0	217	1 HXB7_BOVIN	Q91c89 bos taurus
33	41	100.0	217	1 HXB7_HUMAN	P09629 homo sapien

34	41	100.0	217	1 HXB7_MOUSE	P09024 mus musculu
35	41	100.0	220	1 HB7A_XENLA	Q91771 xenopus lae
36	41	100.0	220	1 HB7B_XENLA	P04776 xenopus lae
37	41	100.0	222	1 HXC5_HUMAN	O00444 homo sapien
38	41	100.0	222	1 HXC5_MOUSE	P32043 mus musculu
39	41	100.0	224	1 HXB6_HUMAN	P17509 homo sapien
40	41	100.0	224	1 HXB6_MOUSE	P09023 mus musculu
41	41	100.0	225	1 BRX1_HUMAN	Q91bui homo sapien
42	41	100.0	225	1 HXA7_MORSA	Q94w44 morone saxa
43	41	100.0	228	1 BRX2_MOUSE	O08686 mus musculu
44	41	100.0	228	1 HXB6_BRARE	P15661 brachydanio
45	41	100.0	229	1 HXA6_HETR	Q91a24 heterodontu

## ALIGNMENTS

```

RESULT 1
HXB6_XENLA          STANDARD;   PRT;   48 AA.
ID   HXB6_XENLA
AC   P31256;
DT   01-JUL-1993 (Rel. 26, Created)
DR   01-JUL-1993 (Rel. 26, Last sequence update)
DI   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Homeobox protein Hox-B6 (XHOX-2.2) (Fragment).
GN   HOB6 OR XHOX-2.2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93043517; PubMed=1384609;
RA   Leroy P., de Robertis E.M.;
RT   "Effects of lithium chloride and retinoic acid on the expression of
RT   genes from the Xenopus laevis Hox 2 complex.";
RL   Dev. Dyn. 194:21-32(1992).
CC   -!- FUNCTION: Sequence-specific transcription factor which is part of
CC   a developmental regulatory system that provides cells with
CC   specific positional identities on the anterior-posterior axis.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the Antp homeobox family.
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@sib-sib.ch).
CC   -----
CC   EMBL, M91587, AAA49750.1; -.
CC   PIR, I51439, I51439.
CC   InterPro, IPR001827, Antennapedia.
CC   InterPro, IPR001356, Homeobox.
CC   Pfam, PF00046, homeobox, 1.
CC   PRINTS, PR00024, HOMEBOX.
CC   ProDom, PD000010, Homeobox, 1.
CC   SMART, SM00389, HOX, 1.
CC   PROSITE, PS00027, HOMEBOX_1, 1.
CC   PROSITE, PS00032, ANTENNAPEDIA, PARTIAL.
CC   PROSITE, PS00071, HOMEBOX_2, 1.
CC   Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC   Transcription regulation.
CC   KW   NON_TER
CC   FT   DNA_BIND
CC   FT   SEQUENCE
CC   SQ   48 AA; 5716 MW; EC39E36822EDDD2A CRC64;
Query Match          100.0%; Score 41; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 RRMKWK 7  
DB 21 RRMKWK 27

## RESULT 2

HXA5\_SHEEP STANDARD; PRT; 49 AA.

AC Q28599;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Homeobox protein Hox-A5 (Fragment).  
GN HOXA5 OR HOXA-5.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxId=9940;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Roche P.J.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Sequence-specific transcription factor which is part of  
CC a developmental regulatory system that provides cells with  
CC specific positional identities on the anterior-posterior axis.  
CC Also binds to its own promoter. Binds specifically to the motif:  
CC 5'-CYAATTA[CG]Y-3'.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: Belongs to the Anp homeobox family.  
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DR EMBL; U61978; AAB04754.1; -.  
DR HSSP; P02833; 1HOM.  
DR InterPro; IPR001356; Homeobox.  
DR Pfam; PF00046; homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS00071; HOMEBOX\_2; 1.  
KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
KW Transcription regulation.  
FT NON\_TER 1  
FT DNA\_BIND <1 49 HOMEBOX.  
FT NON\_TER 49  
SQ SEQUENCE 49 AA; 6331 MW; 1EE702315E7C099B CRC64;

Query Match Best Local Similarity 100.0%; Score 41; DB 1; Length 49;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
DB 41 RRMKWK 47

## RESULT 3

HMA4\_HELTR STANDARD; PRT; 60 AA.

AC P17138;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Homeobox protein HTR-A2 (Fragment).  
OS Helobdella triseriatis (Leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;  
OC Rhynchobdellida; Glossiphoniidae; Helobdella.  
OX NCBI\_TaxId=6413;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Wedeen C.J., Kostriken R.G., Matsunura I., Weisblat D.A.;  
RT "Evidence for a new family of evolutionarily conserved homeobox  
RT genes."  
RL Nucleic Acids Res. 18:1908-1908(1990).  
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -1- SIMILARITY: Contains 1 homeobox domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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DR EMBL; X51752; CA36041.1; -.  
DR PIR; S09227; S09227.  
DR HSSP; P02833; 1SAN.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR000047; HTH\_lambdarepressr.  
DR Pfam; PF00046; homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS00071; HOMEBOX\_2; 1.  
KM Homeobox; DNA-binding; Developmental protein; Nuclear protein.  
FT NON\_TER 1  
FT DNA\_BIND 1 60 HOMEBOX.  
FT NON\_TER 60  
SQ SEQUENCE 60 AA; 7616 MW; 74147P9C6D3814F4 CRC64;

Query Match Best Local Similarity 100.0%; Score 41; DB 1; Length 60;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
DB 52 RRMKWK 58

## RESULT 4

HXA4\_RAT STANDARD; PRT; 67 AA.

AC P09635;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Homeobox protein Hox-A4 (R2) (Fragment).  
GN HOXA4 OR HOX-A4.  
OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=8727429; PubMed=2866401;  
RA Falzon M., Sanderson N., Chung S.Y.;  
RT "Cloning and expression of rat homeo-box-containing sequences."  
RL Gene 54:23-32(1987).

RP SEQUENCE OF 1-42 FROM N.A.  
RX MEDLINE=9521728; PubMed=7702549;  
RA Sakoyama Y., Mizuta I., Ogasawara N., Yoshikawa H.;  
RT "Cloning of rat homeobox genes."

```

RL Biochem. Genet. 32:351-360(1994).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family. Deformed
CC subfamily.
CC -----
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CC -----
CC EMBL; M16808; -; NOT_ANNOTATED_CDS.
CC EMBL; S76296; -; NOT_ANNOTATED_CDS.
CC PIR; B27471; B27471.
CC HSSP; P02833; 9ANT.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRODOM; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00032; ANTENNAPEIDIA; PARTIAL.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS50071; HOMEBOX 2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC NON_TER 1 1
CC DNA_BIND <1 42 HOMEBOX.
CC FT NON_TER 67 67
CC SQ SEQUENCE 67 AA; 8346 MW; 5BFDFAE93193780 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
Db 34 RRMKWK 40

RESULT 5
HXAY_SHEEP
ID HXAY_SHEEP STANDARD; PRT; 71 AA.
AC Q28600;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Fragment).
GN HOXA7 OR HOXA-7.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Roche P.O.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -----
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CC -----
CC EMBL; M84001; AAA49397.1; ALT_INIT.
CC PIR; JC1161; JC1161.
CC HSSP; P02833; ISAN.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRODOM; PD000010; Homeobox; 1.

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CC -----
CC EMBL; U61879; AAB04755.1; -.
CC HSSP; P02833; 9ANT.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR000047; HTH_Lambrpressor.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRINTS; PR00031; HTHREPRESSR.
CC PRODOM; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS50071; HOMEBOX 2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC NON_TER 1 1
CC DNA_BIND 4 63 HOMEBOX.
CC FT NON_TER 71 71
CC SQ SEQUENCE 71 AA; 8888 MW; 931049FAC1BACB7 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
Db 55 RRMKWK 61

RESULT 6
HXCS_NOTVT
ID HXCS_NOTVT STANDARD; PRT; 71 AA.
AC P31262;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-CS (NvHox-3.4) (Fragment).
OS Nototheniidae; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae;
OC Nototheniidae.
OX NCBI_TaxID=8316;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92290273; PubMed=1351019;
RA Belleville S., Beauchemin M., Tremblay M., Noiseux N., Savard P.;
RA "Homeobox-containing genes in the newt are organized in clusters
RA similar to other vertebrates.";
RL Gene 114:179-186(1992).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -----
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CC -----
CC EMBL; M84001; AAA49397.1; ALT_INIT.
CC PIR; JC1161; JC1161.
CC HSSP; P02833; ISAN.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRODOM; PD000010; Homeobox; 1.

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DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.  
 DR PROSITE; PS00071; HOMEBOX 2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Transcription regulation.  
 FT NON\_TER 1  
 FT DNA\_BIND 4  
 FT NON\_TER 71  
 SQ SEQUENCE 71 AA; 8979 MW; 07999FDE8995BA2 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 0.37;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
 Db 55 RRMKWK 61

RESULT 7  
 HMO APIME STANDARD; PRT; 74 AA.  
 AC P15860;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Homeobox protein H90 (Fragment).  
 OS Apis mellifera (Honeybee).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
 OC Apidae; Apis.  
 CC NCBI\_Taxid=7460;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9009384; PubMed=2574865;  
 RA Walldorf U., Fleig R., Gehring W.J.;  
 RT "Comparison of homeobox-containing genes of the honeybee and Drosophila."  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -1- SIMILARITY: Belongs to the Anp homeobox family.  
 CC -1- SIMILARITY: Contains 1 homeobox domain.  
 CC -----  
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 CC -----  
 DR EMBL; M29493; AAA27728.1; -.  
 DR PIR; D14510; D14510.  
 DR HSSP; P02833; 1HOM.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00071; HOMEBOX 2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.  
 FT NON\_TER 1  
 FT DNA\_BIND 8  
 FT NON\_TER 74  
 SQ SEQUENCE 74 AA; 9263 MW; 5FC8BF4F23D3837 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7

Db 59 RRMKWK 65

RESULT 8  
 HMSA SALSA STANDARD; PRT; 75 AA.  
 ID HMSA\_SALSA  
 AC P09636;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Homeobox protein S12A (Fragment).  
 OS Salmo salar (Atlantic salmon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 CC NCBI\_Taxid=8030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88226009; PubMed=2897318;  
 RA Fjose A., Molven A., Eiken H.G.;  
 RT "Molecular cloning and characterization of homeo-box-containing genes from Atlantic salmon."  
 RL Gene 62:141-152(1988).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- SIMILARITY: Belongs to the Anp homeobox family.  
 CC -1- SIMILARITY: Contains 1 homeobox domain.  
 CC -----

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 CC -----  
 DR EMBL; M18903; AAA49559.1; -.  
 DR PIR; I51341; I51341.  
 DR HSSP; P02833; 9ANT.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00071; HOMEBOX 2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.  
 FT NON\_TER 1  
 FT DNA\_BIND 1  
 FT NON\_TER 75  
 SQ SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;

Query Match 100.0%; Score 41; DB 1; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
 Db 52 RRMKWK 58

RESULT 9  
 HXC4 RAT STANDARD; PRT; 76 AA.  
 ID HXC4\_RAT  
 AC P1865;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Homeobox protein Hox-C4 (R3) (Fragment).  
 GN HXC4 OR HXC4-4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=89231502; PubMed=2907739;
RA Falzon M., Chung S.Y.; homeobox-containing genes is developmentally
RT "regulated and tissue specific.";
RL Development 103:601-610(1988).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Predominantly spinal cord and kidney.
CC -1- SIMILARITY: Belongs to the Antp homeobox family. Deformed
CC subfamily.
-----
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DR EMBL: M37567; AAA41343.1; -
DR PIR: C43559; C43559.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_lambdarepressr.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEOBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR PRODOM: PD00010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE: PS00027; HOMEOBOX_1; 1.
DR PROSITE: PS50071; HOMEOBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1
FT DNA_BIND 11
SQ SEQUENCE 76 AA; 9293 MW; 5235F665C0672385 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.4; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 RRMKMKK 7
Db 62 RRMKMKK 68

RESULT 10
HXAS_SALSA STANDARD; PRT; 78 AA.
ID HXAS_SALSA
AC P09637;
DT 01-JAN-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A5 (S12-B) (Fragment).
GN HOXA5.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226009; PubMed=2897318;
RA Jose A., Mølven A., Biken H.G.;
RT "Molecular cloning and characterization of homeo-box-containing genes

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RT from Atlantic salmon.";
RL Gene 62:141-152(1988).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
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DR EMBL: M18904; AAA49560.1; -
DR PIR: I51342; I51342.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEOBOX.
DR PRODOM: PD00010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEOBOX_1; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE: PS50071; HOMEOBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1
FT DNA_BIND 1 60
SQ SEQUENCE 78 AA; 9489 MW; 829DEBDDP78AC820 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.41; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 RRMKMKK 7
Db 52 RRMKMKK 58

RESULT 11
HXAS_LINSA STANDARD; PRT; 80 AA.
ID HXAS_LINSA
AC P81192;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Homeobox protein Hox-A4 (Lshox 4) (Fragment).
GN HOXA4.
OS Linus sanguineus (Ribon worm).
OC Eukaryota; Metazoa; Nemertea; Anopla; Heteronemertea; Lineidae;
OC Linus.
OX NCBI_TaxID=48190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98169491; PubMed=9501210;
RA Kmita-Cunha M., Locoil F., Bierne J., Gehring W.J.;
RT "Homeobox genes in the ribon worm Linus sanguineus: evolutionary
RT implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3030-3035(1998).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the Antp homeobox family. Deformed
CC subfamily.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.

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DR InterPro: IPR000047; HTH_lambdarepressr.
DR Pfam: PF00046; homeobox_1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR PRODOM: PD00010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KM Transcription regulation.
FT NON_TER 1
FT DNA_BIND 21 80 HOMEBOX.
FT NON_TER 80
SQ SEQUENCE 80 AA; 9860 MW; F2CE1B01CB8042F1 CRC64;

Query Match
Best Local Similarity 100.0%; Score 41; DB 1; Length 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
DB 62 RRMKWK 68

RESULT 12
HSL BRARE
ID HSL_BRARE STANDARD; PRT; 81 AA.
AC P09013;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 like (ZF-54) (Fragment).
GN HOXB5 OR ZF54 OR ZF-54.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=8901617; PubMed=2902560;
RA Njlstad P.R., Molven A., Hordvik I., Apold J., Flose A.;
RT "Primary structure, developmentally regulated expression and
RT potential duplication of the zebrafish homeobox gene ZF-21.";
RL Nucleic Acids Res. 16:9097-9113(1988).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12803; CAA31291.1; -
DR HSSP: P02833; ISAN.
DR ZFIN: ZDB-GENE-000823-6; hoxb5b.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRODOM: PD00010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KM Transcription regulation.
FT NON_TER 1

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FT DNA_BIND 6 65 HOMEBOX.
SQ SEQUENCE 81 AA; 9977 MW; B7698AEFFEB3C6B4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 41; DB 1; Length 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
DB 57 RRMKWK 63

RESULT 13
HXB5 CHICK
ID HXB5_CHICK STANDARD; PRT; 82 AA.
AC P14838;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 (Hox-2.1) (Fragment).
GN HOXB5 OR GHOX-2.1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Erythrocyte;
RX MEDLINE=90126373; PubMed=2575515;
RA Madden S.E., Pang K., Eichele G.;
RT "Expression pattern of homeobox-containing genes during chick
RT embryogenesis.";
RL Development 105:639-650(1989).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X16846; CAA34743.1; -
DR PIR: S08302; S08302.
DR HSSP: P02833; ISAN.
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRODOM: PD00010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KM Transcription regulation.
FT NON_TER 1
FT DNA_BIND 7 66 HOMEBOX.
FT NON_TER 1
SQ SEQUENCE 82 AA; 9877 MW; 53F70ACDC9FDEF8F CRC64;

Query Match
Best Local Similarity 100.0%; Score 41; DB 1; Length 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
DB 58 RRMKWK 64

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RESULT 14
HXB6_CHICK
ID HXB6_CHICK STANDARD; PRT; 84 AA.
AC P14839;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (HBOX-2.2) (Fragment).
GN HBOX6 OR HBOX-2.2.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX NCBI_TaxID=9031;
RN SEQUENCE FROM N.A.
RP TISSUE=Erythrocyte;
RX MEDLINE=90126373; PubMed=2575515;
RA Medden S.E., Pang K., Eichele G.;
RT "Expression pattern of homeobox-containing genes during chick
embryogenesis.";
RL Development 105:639-650(1989).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
-----
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-----
CC DR EMBL; X16847; CAA34744.1; -.
CC DR PIR; S08303; S08303.
CC DR HSSP; P02833; 1HOM.
CC DR InterPro; IPR001827; Antennapedia.
CC DR InterPro; IPR001356; Homeobox.
CC DR Pfam; PF00046; homeobox; 1.
CC DR PRINTS; PR00024; HOMEBOX.
CC DR PRINTS; PR00031; HTHREPRESSR.
CC DR ProDom; PD000010; Homeobox; 1.
CC DR SMART; SM00389; HOX; 1.
CC DR PROSITE; PS00027; HOMEBOX_1; 1.
CC DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
CC DR PROSITE; PS00071; HOMEBOX_2; 1.
CC DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC KM Transcription regulation.
CC FT NON_TER 1 1
CC FT DNA_BIND 7 66 HOMEBOX.
CC SQ SEQUENCE 84 AA; 10279 MW; BC06B10165B19E71 CRC64;
-----
Query Match 100.0%; Score 41; DB 1; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RRMKMK 7
DB 58 RRMKMK 64

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RESULT 15
SCR_APIME STANDARD; PRT; 86 AA.
AC P15859;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)

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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein H55 (Fragment).
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OC NCBI_TaxID=7460;
OX NCBI_TaxID=7460;
RN SEQUENCE FROM N.A.
RP MEDLINE=90095384; PubMed=2574865;
RA Walldorf U., Fleig R., Gehring W.J.;
RT "Comparison of homeobox-containing genes of the honeybee and
Drosophila.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY. STRONGEST, TO SCR
OF DROSOPHILA.
-----
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-----
CC DR EMBL; M29488; AAA27723.1; -.
CC DR PIR; A34510; A34510.
CC DR HSSP; P02833; 1SAN.
CC DR InterPro; IPR001827; Antennapedia.
CC DR InterPro; IPR001356; Homeobox.
CC DR Pfam; PF00046; homeobox; 1.
CC DR PRINTS; PR00024; HOMEBOX.
CC DR ProDom; PD000010; Homeobox; 1.
CC DR SMART; SM00389; HOX; 1.
CC DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
CC DR PROSITE; PS00027; HOMEBOX_1; 1.
CC DR PROSITE; PS00071; HOMEBOX_2; 1.
CC DR Homeobox; DNA-binding; Developmental protein; Nuclear protein.
CC KM Non-TER 1 1
CC FT DNA_BIND 8 67 HOMEBOX.
CC FT NON_TER 86 86
CC SQ SEQUENCE 86 AA; 10713 MW; 2A49AB857C138AB8 CRC64;
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Query Match 100.0%; Score 41; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RRMKMK 7
DB 59 RRMKMK 65

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Search completed: August 11, 2004, 14:01:01
Job time : 14 secs

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OM protein - protein search, using sw model

Run on: August 11, 2004, 13:58:07; Search time 36 Seconds

(without alignments)  
61.351 Million cell updates/sec

Title: US-09-854-204-2

Perfect score: 41

Sequence: 1 RRMKWK 7

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	30	13	Q86FV5
2	41	100.0	33	5	Q86FV5
3	41	100.0	39	6	Q9XN68
4	41	100.0	39	13	Q57368
5	41	100.0	42	11	Q80WH6
6	41	100.0	43	13	Q57359
7	41	100.0	44	5	Q8GR21
8	41	100.0	46	13	Q9PVR9
9	41	100.0	51	5	Q27413
10	41	100.0	51	5	Q23743
11	41	100.0	51	5	Q26407
12	41	100.0	57	13	Q9PVR8
13	41	100.0	58	5	Q9Y188
14	41	100.0	58	5	Q25208
15	41	100.0	58	13	Q57362
16	41	100.0	59	5	Q8WRW9

17	41	100.0	59	5	Q9NB42	Q9nb42 anopheles g
18	41	100.0	59	13	Q9PVR5	Q9pvr5 oryzias lat
19	41	100.0	60	5	Q77143	Q77143 archegozete
20	41	100.0	60	5	Q77139	Q77139 archegozete
21	41	100.0	60	5	Q97219	Q97219 branchiosto
22	41	100.0	60	5	Q26375	Q26375 styela clat
23	41	100.0	60	11	Q80WH7	Q80wh7 rattus sp.
24	41	100.0	60	11	Q80WH4	Q80wh4 rattus sp.
25	41	100.0	60	11	Q80WH3	Q80wh3 rattus sp.
26	41	100.0	60	11	Q80WH2	Q80wh2 rattus sp.
27	41	100.0	60	13	Q9PSZ1	Q9ps21 petromyzon
28	41	100.0	60	13	Q8QGL9	Q8qgl9 petromyzon
29	41	100.0	60	13	Q8QGL5	Q8qgl5 petromyzon
30	41	100.0	60	13	Q8QGL3	Q8qgl3 petromyzon
31	41	100.0	60	13	Q8QGL6	Q8qgl6 petromyzon
32	41	100.0	60	13	Q8QGL2	Q8qgl2 petromyzon
33	41	100.0	60	13	Q91769	Q91769 xenopus lae
34	41	100.0	60	13	Q8QGL8	Q8qgl8 petromyzon
35	41	100.0	60	13	Q9PSZ2	Q9ps22 petromyzon
36	41	100.0	60	13	Q8QGL7	Q8qgl7 petromyzon
37	41	100.0	61	5	Q27910	Q27910 polyanthroca
38	41	100.0	63	5	Q8MKX2	Q8mkx2 holopneuste
39	41	100.0	63	5	Q8MKX2	Q8mkx2 holopneuste
40	41	100.0	66	13	Q57356	Q57356 brachydantio
41	41	100.0	69	5	Q963K9	Q963k9 phascollion
42	41	100.0	69	5	Q9U9T4	Q9u9t4 nereis vire
43	41	100.0	69	5	Q9BME7	Q9bme7 halictis as
44	41	100.0	69	13	Q9PVR3	Q9pvr3 oryzias lat
45	41	100.0	70	5	Q967W5	Q967w5 folsomia ca

#### ALIGNMENTS

RESULT 1	Q86FV5	PRELIMINARY;	PRT;	30 AA.
AC	Q86FV5			
DT	01-JUN-2002 (TREMBLER1, 21, Created)			
DT	01-JUN-2002 (TREMBLER1, 21, Last sequence update)			
DT	01-JUN-2003 (TREMBLER1, 24, Last annotation update)			
DE	Homeobox protein Hox1s (Fragment).			
OS	Lampetra fluviatilis (River lamprey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypercoartia;			
OC	Petromyzontiformes; Petromyzontidae; Lampetra.			
OX	NCBI_taxid=7748;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21918662; PubMed=11919618;			
RA	Cohn M.J.;			
RL	"Evolutionary biology: Lamprey Hox genes and the origin of jaws.";			
RT	Nature 416:386-387(2002).			
DR	EMBL; AY089981; AAM09102.1; -.			
DR	GO; GO:0005634; C:nucleus; IEA.			
DR	GO; GO:0003700; F:transcription factor activity; IEA.			
DR	GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.			
DR	InterPro; IPR001356; Homeobox.			
DR	Pfam; PF00045; homeobox_1.			
DR	PROSITE; PS00071; HOMEBOX_2; 1.			
FT	NON_TER			
FT	NON_TER			
SC	SEQUENCE 30 AA; 3608 MM; 478B2DF581E5C8E0 CRC64;			
Query Match	100.0%; Score 41; DB 13; Length 30;			
Best local similarity	100.0%; Pred. No. 1.1;			
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 RRMKWK 7			
DB	6 RRMKWK 12			
RESULT 2	Q86FV5			

```

ID 086FU0 PRELIMINARY; PRT; 33 AA.
AC 086FU0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Antennapedia complex (Fragment).
GN ANT-C.
OS Drosophila pseudobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93292933; PubMed=8099892;
RA Randazzo F.M., Seeger M.A., Huss C.A., Sweeney M.A., Cecil J.K.,
RA Kaufman T.C.;
RT "Structural changes in the antennapedia complex of Drosophila
RT pseudobscura."
RL Genetics 134:319-330(1993).
DR EMBL; S63455; AAPI3946.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
FT NON_TER
FT 1
FT 33
SQ SEQUENCE 33 AA; 3863 MW; D78B37ED81PD45DF CRC64;

Query Match 100.0%; Score 41; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7
DB 16 RRMKKK 22

RESULT 3
QXRT68 PRELIMINARY; PRT; 39 AA.
ID 09XT68;
AC 09XT68;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hoxa (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99265967; PubMed=10331940;
RA Li R., Mignot E., Parraco J., Kadotani H., Cantanese J., Zhao B.,
RA Lin X., Hinton L., Ostrander E.A., Patterson D.F., de Jong P.T.;
RT "Construction and characterization of an eightfold redundant dog
RT genomic bacterial artificial chromosome library."
RL Genomics 58:9-17(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Kadotani H., Mignot E.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF103746; AAD40572.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.

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DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
FT DNA-binding; Homeobox; Nuclear protein.
FT NON_TER
FT 1
FT 39
SQ SEQUENCE 39 AA; 4908 MW; 1252D75EA245BCAB CRC64;

Query Match 100.0%; Score 41; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7
DB 22 RRMKKK 28

RESULT 4
QXRT68 PRELIMINARY; PRT; 39 AA.
ID 057368;
AC 057368;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hoxc protein (Fragment).
DE HOXC5A OR HOXC5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "zebrafish hox genes: genomic organization and modified colinear
RT expression patterns in the trunk."
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14539; CAAT4874.1; -
DR ZFIN; ZDB-GENE-980526-533; hoxc5a.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR00047; HTH lambridepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER
FT 1
FT 39
SQ SEQUENCE 39 AA; 4827 MW; 592A0FEC12B58660 CRC64;

Query Match 100.0%; Score 41; DB 13; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7
DB 23 RRMKKK 29

RESULT 5
QXRT68 PRELIMINARY; PRT; 42 AA.
ID 080WH6;
AC 080WH6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

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DE Hox-A|Hox-1 (Fragment).  
 GN Hox-A|Hox-1.  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10118;  
 RX MEDLINE=95217128; PubMed=7702549;  
 RA Sakayama Y., Mizuta I., Ogasawara N., Yoshikawa H.;  
 RT "Cloning of rat homeobox genes."  
 RL Biochem. Genet. 32:351-360(1994).  
 DR EMBL: S76290; AABJ1864.1; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; homeobox\_1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR PRINTS: PR00031; HTHREPRESSR.  
 DR ProDom: PD00010; Homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR PROSITE: PS00027; HOMEBOX\_1; 1.  
 DR PROSITE: PS50071; HOMEBOX\_2; 1.  
 FT NON\_TER 1 42 1  
 FT SEQUENCE 42 AA; 5494 MW; 38515392216FB9 CRC64;  
 SQ  
 Query Match 100.0%; Score 41; DB 11; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
 DB 34 RRMKMK 40  
 ID 057359 PRELIMINARY; PRT; 43 AA.  
 AC 057359;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Hox5 protein (Fragment).  
 GN Hox5B OR HOXA5.  
 OS Brachydanio reio (Zebrafish) (Danio reio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;  
 RT "Zebrafish hox genes: genomic organization and modified colinear  
 expression patterns in the trunk."  
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: Y14526; CAA74861.1; -.  
 DR ZFIN: ZDB-GENE-000823-6; hox5b.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; homeobox; 1.  
 DR PRINTS: PD00010; Homeobox.  
 DR ProDom: PD000024; Homeobox; 1.  
 DR PROSITE: PS00027; HOMEBOX\_1; 1.  
 DR PROSITE: PS50071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kondo S., Naruse K., Shima A.;  
 SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;  
 SQ

Query Match 100.0%; Score 41; DB 13; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
 DB 19 RRMKMK 25  
 ID 09GR21 PRELIMINARY; PRT; 44 AA.  
 AC 09GR21;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Hox type homeodomain protein (Fragment).  
 GN ANTHOX1A.  
 OS Nematostella vectensis.  
 OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actinoptera;  
 OC Eudartarida; Nemertostella.  
 NCBI\_TaxID=45351;  
 RX MEDLINE=97435515; PubMed=9290214;  
 RA Finerty J.R., Martindale M.O.;  
 RT "Homeoboxes in sea anemones (Cnidaria:Anthozoa): a PCR-based survey of  
 Nematostella vectensis and Metridium senile."  
 RL Biol. Bull. 193:62-76(1997).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: AF020955; AAG37788.1; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; Homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR ProDom: PD00010; Homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR PROSITE: PS00027; HOMEBOX\_1; 1.  
 DR PROSITE: PS50071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kondo S., Naruse K., Shima A.;  
 SQ SEQUENCE 44 AA; 5362 MW; FAF8044070A9CCF3 CRC64;  
 SQ

Query Match 100.0%; Score 41; DB 5; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
 DB 20 RRMKMK 26  
 ID 09PVR9 PRELIMINARY; PRT; 46 AA.  
 AC 09PVR9;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE HOXA5A (Fragment).  
 GN HOXA5A.  
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
 OC Belontiiformes; Atherinichthyidae; Oryziatidae; Oryzias.  
 NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kondo S., Naruse K., Shima A.;  
 SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;  
 SQ

RT "Hox genes of the medakafish *Oryzias latipes*.";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: AB026960; BAA86243.1; -.  
 DR HSSP: P02833; 1HOM.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; P:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX; 1.  
 DR ProDom: PD000010; Homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR PROSITE: PS00027; HOMEBOX 1; 1.  
 DR PROSITE: PS50071; HOMEBOX 2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 46 AA; 5955 MW; 6039999ED4294DD3 CRC64;  
 Query Match 100.0%; Score 41; DB 13; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 1.6; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKWK 7  
 DB 32 RRMKWK 38  
 RESULT 9  
 ID Q27413 PRELIMINARY; PRT; 51 AA.  
 AC Q27413;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE LOX5 ORTHOLOG homeobox (Fragment).  
 GN CTS-LOX5.  
 OS Ctenodrilus serratus.  
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;  
 OC Terebellida; Ctenodrilidae; Ctenodrilus.  
 OC NCBI\_TaxID=40316;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94356262; PubMed=7915607;  
 RA Dick M.H., Buss L.W.;  
 RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus  
 (Annelida: Polychaeta).";  
 RL Mol. Phylogenet. Evol. 3:146-158(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Dick M.H., Buss L.W.;  
 RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: U26629; AAC46851.1; -.  
 DR EMBL: 576226; AAC31777.1; -.  
 DR HSSP: P02833; 9ANT.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; P:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR ProDom: PD000010; Homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR PROSITE: PS00027; HOMEBOX 1; 1.  
 DR PROSITE: PS50071; HOMEBOX 2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 51 AA; 6278 MW; 88C6F65161E94A22 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKWK 7  
 DB 32 RRMKWK 38  
 RESULT 10  
 ID Q23743 PRELIMINARY; PRT; 51 AA.  
 AC Q23743;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Deformed ortholog homeobox (Fragment).  
 GN CTS-DFD.  
 OS Ctenodrilus serratus.  
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;  
 OC Terebellida; Ctenodrilidae; Ctenodrilus.  
 OC NCBI\_TaxID=40316;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94356262; PubMed=7915607;  
 RA Dick M.H., Buss L.W.;  
 RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus  
 (Annelida: Polychaeta).";  
 RL Mol. Phylogenet. Evol. 3:146-158(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Dick M.H., Buss L.W.;  
 RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: U26627; AAC46849.1; -.  
 DR HSSP: P02833; 9ANT.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; P:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR ProDom: PD000010; Homeobox; 1.  
 DR PROSITE: PS00027; HOMEBOX 1; 1.  
 DR PROSITE: PS50071; HOMEBOX 2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 51 AA; 6533 MW; 9EDB50C927F8CBDS CRC64;  
 Query Match 100.0%; Score 41; DB 5; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKWK 7  
 DB 32 RRMKWK 38  
 RESULT 11  
 ID Q26407 PRELIMINARY; PRT; 51 AA.  
 AC Q26407;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE CTS-dfd protein (Fragment).  
 GN CTS-DFD.  
 OS Ctenodrilus serratus.  
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;  
 OC Terebellida; Ctenodrilidae; Ctenodrilus.

OX NCBI\_TaxID=40316;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94356262; PubMed=7915607;  
RA Dick M.H., Buss L.W.,  
RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus  
RL (Annelida: Polychaeta)."  
CC Mol. Phylogenet. Evol. 3:146-158(1994).  
DR EMBL: S76416; AAB31775.1; -.  
DR HSSP: P02833; 9ANT.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR001356; Homeobox.  
DR InterPro: IPR000047; HTH\_lambdarepressr.  
DR Pfam: PF00046; homeobox; 1.  
DR PRINTS: PR00024; HOMEBOX.  
DR PRINTS: PR00031; HTHREPRESSR.  
DR ProDom: PD000010; Homeobox; 1.  
DR SMART: SM00389; HOX; 1.  
DR PROSITE: PS00027; HOMEBOX\_1; 1.  
DR PROSITE: PS50071; HOMEBOX\_2; 1.  
KM DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER  
SQ SEQUENCE 51 AA; 653 MW; 9EDB50C927FBCBD5 CRC64;  
  
Query Match 100.0%; Score 41; DB 5; Length 51;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RRMKMK 7  
DB 32 RRMKMK 38  
  
RESULT 12  
ID Q9YV8 PRELIMINARY; PRT; 57 AA.  
AC Q9YV8;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE HOXA5A (Fragment).  
GN HOXA5A.  
OS Oryzias latipes (Medaka fish) (Japanese ricefish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.  
OX NCBI\_TaxID=8090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kondo S., Naruse K., Shima A.,  
RT Hox genes of the medakafish Oryzias latipes."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL: AB026961; BAA86244.1; -.  
DR HSSP: P02833; 1HOM.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR001356; Homeobox.  
DR Pfam: PF00046; homeobox; 1.  
DR PRINTS: PR00024; HOMEBOX.  
DR ProDom: PD000010; Homeobox; 1.  
DR SMART: SM00389; HOX; 1.  
DR PROSITE: PS00027; HOMEBOX\_1; 1.  
DR PROSITE: PS50071; HOMEBOX\_2; 1.  
KM DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER  
SQ SEQUENCE 57 AA; 6891 MW; 5AA6430320F68C04 CRC64;

Query Match 100.0%; Score 41; DB 13; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RRMKMK 7  
DB 32 RRMKMK 38  
  
RESULT 13  
ID Q9Y188 PRELIMINARY; PRT; 58 AA.  
AC Q9Y188;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE HBI homeodomain protein (Fragment).  
GN HBI.  
OS Priapulus caudatus.  
OC Eukaryota; Metazoa; Priapulida; Priapulidae; Priapulidae.  
OX NCBI\_TaxID=37621;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99318125; PubMed=10391241;  
RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,  
RT "Hox genes in brachiopods and priapulids and protostome evolution."  
RL Nature 399:772-776(1999).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL: AF144888; AAD04644.1; -.  
DR HSSP: P02833; 9ANT.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR001356; Homeobox.  
DR InterPro: IPR000047; HTH\_lambdarepressr.  
DR Pfam: PF00046; homeobox; 1.  
DR PRINTS: PR00024; HOMEBOX.  
DR PRINTS: PR00031; HTHREPRESSR.  
DR ProDom: PD000010; Homeobox; 1.  
DR SMART: SM00389; HOX; 1.  
DR PROSITE: PS00027; HOMEBOX\_1; 1.  
DR PROSITE: PS50071; HOMEBOX\_2; 1.  
KM DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER  
SQ SEQUENCE 58 AA; 7323 MW; 572F30DA57C9A613 CRC64;  
  
Query Match 100.0%; Score 41; DB 5; Length 58;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RRMKMK 7  
DB 33 RRMKMK 39  
  
RESULT 14  
ID Q25208 PRELIMINARY; PRT; 58 AA.  
AC Q25208;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Antennapedia protein (Fragment).  
GN ANTENNAPEDIA.  
OS Junonia coenia (Peacock butterfly) (Precis coenia).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditytista;  
OC Papilionidae; Nymphalidae; Nymphalinae; Junonia.  
OX NCBI\_TaxID=39708;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95075456; PubMed=7840822;

RA Warren R.W., Nagy L., Selegue J., Gates J., Carroll S.,  
 RT "Evolution of homeotic gene regulation and function in flies and  
 RT butterflies".  
 RL Nature 372:458-461 (1994).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; L42135; AA68461.1; -.  
 DR PIR; S58850; S58850.  
 DR HSSP; P02833; 1HOM.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; P:regulation of transcription factor activity; IEA.  
 DR GO; GO:0003355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR000047; HTH\_LambdaRepressr.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HTHREPRESSR.  
 DR PRINTS; PR00031; HTHREPRESSR.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00388; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1  
 FT NON\_TER 58  
 SQ SEQUENCE 58 AA; 7583 MW; BD69B4875BAE565E CRC64;  
 Query Match 100.0%; Score 41; DB 5; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKKKK 7  
 DB 52 RRMKKKK 58  
 RESULT 15  
 ID 057362 PRELIMINARY; PRT; 58 AA.  
 AC 057362;  
 DT 01-JUN-1998 (TREMblrel. 06, Created)  
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)  
 DE Hoxb7 protein (Fragment).  
 GN HOXB7A OR HOXB7.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;  
 RT "Zebrafish hox genes: genomic organization and modified colinear  
 RT expression patterns in the trunk".  
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; Y14533; CAAT4868.1; -.  
 DR TRANSFAC; T03635; -.  
 DR ZFIN; ZDB-GENE-000329-2; hoxb7a.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; P:regulation of transcription factor activity; IEA.  
 DR GO; GO:0003355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR000047; HTH\_LambdaRepressr.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRINTS; PR00031; HTHREPRESSR.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00388; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1  
 FT NON\_TER 58  
 SQ SEQUENCE 58 AA; 6863 MW; 41EA6F1448DA1E5 CRC64;

Query Match 100.0%; Score 41; DB 13; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
 DB 23 RRMKKKK 29

Search completed: August 11, 2004, 14:01:48  
 Job time : 37 secs





CC amino acid substitutions. See GENESEQ records MAY83520-Y83581  
 XX Sequence 7 AA;  
 SO Query Match 100.0%; Score 41; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKMKK 7  
 DB 1 RRMKMKK 7

RESULT 2  
 ADE14786  
 ID ADE14786 standard; peptide; 7 AA.  
 XX ADE14786;  
 AC ADE14786;  
 XX 29-JAN-2004 (first entry)  
 DE Carrier moiety SeqID6 related to improved drug delivery.  
 XX drug delivery system; carrier group; homeobox peptide; drug metabolism;  
 KM drug biotransformation; drug excretion; drug half life; drug solubility;  
 KM drug side-effect; drug resistance; penatrin; antennapedia homeodomain;  
 KM fruit fly; mutant; mutain.  
 XX Synthetic.  
 OS Drosophila melanogaster.  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "Optionally C-terminal H"  
 FT Modified-site 7 /note= "N-terminal amide"  
 FT Modified-site 7 /note= "N-terminal amide"  
 PN WO200001417-A1.  
 XX 13-JAN-2000.  
 PD 22-JUN-1999; 99WO-GB001957.  
 XX 03-JUL-1998; 98GB-00014527.  
 PR (CYCL-) CYCLACEL LTD.  
 PA Fischer PM, Wang S;  
 XX WPI; 2000-160729/14.  
 DR WPI; 2000-160729/14.  
 XX Delivery systems with improved delivery into target cells, half-life,  
 PT solubility in biological fluids, enhanced metabolism, biotransformation and  
 PT excretion, and minimal toxic side-effects.  
 XX Claim 33; SEQ ID NO 26; 114pp; English.

This invention relates to novel drug delivery systems comprising a drug group linked to a carrier group comprising a homeobox peptide, its fragment or derivative. The invention may provide a method of improved delivery into target cells with enhanced metabolism, biotransformation and excretion of a drug. The drug may be therapeutically active in both intact and dissociated states. The invention may improve half-life of a drug in human or animal bodies, improve solubility in biological fluids, minimize known toxic or non-desirable side-effects, enhance onset of action of a desired therapeutic effect, provide alternative routes for administration of drug and decrease incidence of drug resistance. The present sequence is the amino acid sequence of a carrier peptide derived from penatrin, a peptide derived from the antennapedia homeodomain of Drosophila melanogaster. The drug and carrier moieties associated with this sequence in the exemplification of the invention are featured.

Sequence 7 AA;

Query Match 100.0%; Score 41; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKMKK 7  
 DB 1 RRMKMKK 7

RESULT 3  
 ADE14762  
 ID ADE14762 standard; peptide; 7 AA.  
 XX ADE14762;  
 AC ADE14762;  
 XX 29-JAN-2004 (first entry)  
 DE Drosophila melanogaster homeodomain truncated penatrin peptide SeqID2.  
 XX drug delivery system; carrier group; homeobox peptide; drug metabolism;  
 KM drug biotransformation; drug excretion; drug half life; drug solubility;  
 KM drug side-effect; drug resistance; penatrin; antennapedia homeodomain;  
 KM fruit fly.  
 XX Drosophila melanogaster.  
 OS Drosophila melanogaster.  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "Optionally C-terminal H"  
 FT Modified-site 7 /note= "N-terminal amide"  
 FT Modified-site 7 /note= "N-terminal amide"  
 PN WO200001417-A1.  
 XX 13-JAN-2000.  
 PD 22-JUN-1999; 99WO-GB001957.  
 XX 03-JUL-1998; 98GB-00014527.  
 PR (CYCL-) CYCLACEL LTD.  
 PA Fischer PM, Wang S;  
 XX WPI; 2000-160729/14.  
 DR WPI; 2000-160729/14.  
 XX Delivery systems with improved delivery into target cells, half-life,  
 PT solubility in biological fluids, enhanced metabolism, biotransformation and  
 PT excretion, and minimal toxic side-effects.  
 XX Claim 9; SEQ ID NO 2; 114pp; English.

This invention relates to novel drug delivery systems comprising a drug group linked to a carrier group comprising a homeobox peptide, its fragment or derivative. The invention may provide a method of improved delivery into target cells with enhanced metabolism, biotransformation and excretion of a drug. The drug may be therapeutically active in both intact and dissociated states. The invention may improve half-life of a drug in human or animal bodies, improve solubility in biological fluids, minimize known toxic or non-desirable side-effects, enhance onset of action of a desired therapeutic effect, provide alternative routes for administration of drug and decrease incidence of drug resistance. The present sequence is the amino acid sequence of a truncated form of penatrin, a peptide derived from the antennapedia homeodomain of Drosophila melanogaster, which is related to the invention.

Sequence 7 AA;

Query Match 100.0%; Score 41; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKMKK 7  
 DB 1 RRMKMKK 7

RESULT 4

ABG75504  
AC ABG75504;  
DT 14-APR-2003 (first entry)  
DE Fruit fly Antp-HD truncated membrane translocation sequence #2.  
KW Translocation; delivery vehicle; agent-membrane translocation sequence;  
KW MTS; membrane translocation sequence; plasma membrane; red blood cell;  
KW immunisation; antigen; intracellular delivery; therapeutic; HIV-1;  
KW trans-activating protein; Tat; Antennapedia homeodomain protein; Antp-HD;  
KW VP22 protein; HSV-VP22; signal-sequence-based peptide; Transportan;  
KW Amphiphilic model peptide; Fruit fly.  
OS Drosophila sp.  
PN US2002151004-A1.  
PD 17-OCT-2002.  
XX 16-FEB-2001; 2001US-00785802.  
XX 24-JUL-2000; 2000WO-GB002848.  
XX 09-AUG-2000; 2000WO-GB003056.  
PR 22-DEC-2000; 2000US-00748063.  
PR 22-DEC-2000; 2000US-00748789.  
XX (CRAI/) CRAIG R.  
PA Craig R;  
XX WPI; 2002-280593/32.  
DR Preparing a red blood cell vehicle suitable for delivering an agent to a  
PT target site in a vertebrate due to loading the red blood cell with an  
PT agent-membrane translocation sequence.  
XX  
XX Disclosure; Page 8; 43pp; English.  
XX The invention discloses a method for preparing a delivery vehicle for  
CC delivering an agent to a target site in a vertebrate. The method  
CC comprises loading a cell with an agent-membrane translocation sequence  
CC (MTS) conjugate, which contains a membrane translocation sequence  
CC enabling the agent to cross the plasma membrane of a cell. Also disclosed  
CC is a pharmaceutical composition comprising a red blood cell for delivery  
CC of an agent to a vertebrate, the red blood cell comprising the novel  
CC agent-MTS conjugate and a method of immunisation of an animal with an  
CC antigen. The method is useful for preparing delivery vehicles,  
CC particularly a red blood cell, for the intracellular delivery of a  
CC therapeutic agent to a target site. The method is particularly useful for  
CC enabling an agent to cross the plasma membrane of a target cell, and for  
CC selectively releasing the agent-MTS conjugate at a target site to  
CC facilitate the uptake of the agent by the cells at the target site. The  
CC preferred MTS sequences are from HIV-1 trans-activating protein (Tat),  
CC Drosophila Antennapedia homeodomain protein (Antp-HD), Herpes Simplex-1  
CC virus VP22 protein (HSV-VP22), a signal-sequence-based peptide and a  
CC Transportan and Amphiphilic model peptide. The sequence presented is the  
CC active truncated Fruit fly MTS, #2  
XX  
XX Sequence 7 AA;  
SO

Query Match 100.0%; Score 41; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.44+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID	AAE17558	standard; peptide; 7 AA.
XX	AAE17558;	
XX	22-APR-2002	(first entry)
XX	Fluorescent timer fusion proteins constructing NLS peptide #16.	
XX	Fluorescent timer protein; protein movement; translocation; trafficking;	
XX	promoter activity; gene expression; transgenic plant; gene modification;	
XX	protein age; nuclear localisation signal; NLS.	
XX	Unidentified.	
XX	MO200196373-A2.	
XX	20-DEC-2001.	
XX	13-JUN-2001; 2001WO-US019097.	
XX	14-JUN-2000; 2000US-0211607P.	
XX	(CLON-) CLONTECH LAB INC.	
XX	Pradkov AF, Tersikh A;	
XX	WPI; 2002-154595/20.	
XX	New fluorescent timer proteins comprising an emission spectrum that	
XX	changes over time from a first wavelength to a second wavelength, useful	
XX	for monitoring intracellular protein movement, translocation, trafficking	
XX	or stability.	
XX	Disclosure; Page 18; 89pp; English.	
XX	The invention relates to a fluorescent timer protein having an emission	
XX	spectrum that changes over time after synthesis from a first wavelength	
XX	to a second wavelength. The fluorescent timer proteins are useful in	
XX	monitoring the activity of a promoter, determining the age of a protein,	
XX	identifying an agent that modulates the activity of a promoter and in	
XX	enriching a population of cells comprising a fluorescent timer protein.	
XX	The fluorescent timer proteins are also useful for assessing gene	
XX	expression during development of a multicellular organism or during	
XX	cellular differentiation, in response to a drug or other inducer of	
XX	promoter activity, as a reporter to serve as a read-out of promoter	
XX	activity, monitoring intracellular protein movement or translocation,	
XX	protein trafficking, or protein stability, to investigate temporal	
XX	aspects of the activity of a regulatory element, for determining cell	
XX	fate during development and organ remodeling, in spatial and temporal	
XX	visualisation of newly synthesised proteins and accumulated proteins, and	
XX	in distinguishing between newly formed and pre-existing structures, e.g.	
XX	membrane junctions and extracellular matrix components. The fluorescent	
XX	timer proteins may further be used to investigate where photobleaching	
XX	techniques are employed, as detectable labels, as selectable markers, as	
XX	biosensors in prokaryotic and eukaryotic cells, in protease cleavage	
XX	assays, and as second messenger detectors. The nucleic acids can be used	
XX	to generate transgenic, non-human plants or animals or site-specific gene	
XX	modifications in cell lines. The present sequence is nuclear localisation	
XX	signal (NLS) peptide used for constructing fluorescent timer proteins	
XX	Sequence 7 AA;	
XX	Query Match	100.0%; Score 41; DB 5; Length 7;
XX	Best Local Similarity	100.0%; Pred. No. 1.4e+06;
XX	Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

## RESULT 5

## RESULT 6

AA048627  
ID AA048627 standard; peptide; 7 AA.  
XX  
AC AA048627;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 130.  
XX  
KW Antinflammatory; antiaesthetic; cytosolic; antiproliferative; neurotropic;  
KW antineumatic; antiaesthetic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW allergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014346.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PR 22-AUG-2000; 2000US-00643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
XX  
PA (UYVA) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel antinflammatory compound comprising membrane translocation domain  
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
PT activation, and for treating asthma, lung inflammation, psoriasis.  
XX  
PS Claim 11; Page 62; 88pp; English.  
XX  
CC The invention relates to an antinflammatory compound (especially  
CC AA048628-AA048645), comprising a membrane translocation domain (AA048620-  
CC AA048627 or AA048646-AA048651) which comprises from 6-15 amino acid  
CC residues, fused to a NEMO binding sequence (AA048525-AA048619). The  
CC antinflammatory compounds have antiaesthetic, cytostatic, antiproliferative,  
CC immunosuppressive, dermatological, neuroprotective, nootropic,  
CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis  
XX  
SQ Sequence 7 AA:  
XX  
Query Match 100.0%; Score 41; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 RRMKXK 7  
RESULT 7  
AA048620  
ID AA048620 standard; peptide; 7 AA.  
XX  
AC AA048620;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 123.  
XX  
KW Antinflammatory; antiaesthetic; cytosolic; antiproliferative; neurotropic;  
KW antineumatic; antiaesthetic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW allergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014346.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PR 22-AUG-2000; 2000US-00643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
XX  
PA (UYVA) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel antinflammatory compound comprising membrane translocation domain  
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
PT activation, and for treating asthma, lung inflammation, psoriasis.  
XX  
PS Claim 11; Page 62; 88pp; English.  
XX  
CC The invention relates to an antinflammatory compound (especially  
CC AA048628-AA048645), comprising a membrane translocation domain (AA048620-  
CC AA048627 or AA048646-AA048651) which comprises from 6-15 amino acid  
CC residues, fused to a NEMO binding sequence (AA048525-AA048619). The  
CC antinflammatory compounds have antiaesthetic, cytostatic, antiproliferative,  
CC immunosuppressive, dermatological, neuroprotective, nootropic,  
CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis  
XX  
SQ Sequence 7 AA:  
XX  
Query Match 100.0%; Score 41; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7  
1 RRMKKK 7  
DB 1 RRMKKK 7

## RESULT 8

ABP60478  
ID ABP60478 standard; peptide; 7 AA.

ABP60478;  
10-MAY-2003 (first entry)  
NLS peptide SEQ ID NO 17.  
Protease; detection; drug screening; caspase; apoptosis; infection;  
nuclear localisation signal; NLS.

Unidentified.

WO2003012393-A2.

13-FEB-2003.

30-JUL-2002; 2002WO-US024119.

31-JUL-2001; 2001US-0309312P.

(CLON-) CLONTECH LAB INC.

Haugwitz M;

WPI; 2003-248202/24.

Detecting the presence of active protease in a cell for use in protease activity detection and drug screening applications, by using a protease detection fusion protein.

Disclosure; Page 10; 43pp; English.

The invention relates to a cell comprising a protease detection fusion protein containing first and second subcellular localisation domains (D1, D2) separated by a cleavage domain (CD) recognised by the protease, (where D1 is dominant over D2 and a label domain is present between CD and D2). The fusion protein is maintained for a period of time sufficient for CD to be cleaved by protease if present in the cell and subcellular location of label domain is detected. The method is useful for determining whether a cell contains an active protease. The method finds applications, including monitoring activity of a protease in a cell, monitoring the effect of an agent on the activity of a protease, e.g. for drug screening applications to identify agents that modulate the activity of a particular protease and studying the effect of a factor on expression of the protease-encoding gene. Detecting protease activity of interest in a cell is useful for determining the particular state of the cell associated with the particular protease, e.g. certain active caspases indicate that a cell is undergoing an apoptotic event. Protease detection applications can be used in diagnostic applications, including diagnosis of bacterial and/or viral pathogenic infection. The present sequence is that of a nuclear localisation signal (NLS) containing peptide disclosed in illustrations of the invention

Sequence 7 AA;

Query Match 100.0%; Score 41; DB 6; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7  
1 RRMKKK 7  
DB 1 RRMKKK 7

## RESULT 9

ABP96972  
ID ABP96972 standard; peptide; 7 AA.

ABP96972;

17-JUN-2003 (first entry)

Anti-inflammatory polypeptide SEQ ID NO:11.

Anti-inflammatory; inflammatory disorder; polybasic; antiaesthetic; cyostatic; tuberculostatic; nephrotoxic; antineuritic; antiaesthetic; dermatological; immunosuppressive; antiallergic; antiparasitic; asthma; gynaecological; ophthalmological; thrombolytic; protein therapy; lung inflammation; cancer; chronic granulomatous disease; tuberculosis; leprosy; sarcoidosis; silicosis; nephritis; rheumatoid arthritis; amyloidosis; ankylosing spondylitis; chronic bronchitis; scleroderma; lupus; appendicitis; psoriasis; pelvic inflammatory disease; allergy; orbital inflammatory disease; thrombotic disease.

Synthetic.

WO2003020213-A2.

13-MAR-2003.

27-AUG-2002; 2002WO-US027421.

30-AUG-2001; 2001US-0316328P.

(PRAE-) PRAECTIS PHARM INC.

Lazarus D, Hannig G;

WPI; 2003-354457/33.

New polypeptide useful for treating inflammatory disorders, such as asthma, lung inflammation, cancer, chronic granulomatous diseases, nephritis, amyloidosis, rheumatoid arthritis, scleroderma or allergies.

Claim 34; Page 23; 35pp; English.

The present invention describes an anti-inflammatory compound comprising a polybasic peptide (I). (I) comprises the structure: B1-X1-X2-X3-B2-X4-X5-B3; or B1-X1-X2-B2-B3-X3-X4-B4, where B1, B2, B3 and B4 = basic amino acid residues; and X1, X2, X3, X4 and X5 = alpha-helix promoting amino acid residues. Also described: (1) methods of treating an inflammatory disorder in a subject; and (2) a method for modulating the secretion of pro-inflammatory cytokines in a cell. (1) has cyostatic, antineuritic, antiallergic, antiparasitic, dermatological, immunosuppressive, antineuritic, antiallergic, antiparasitic, dermatological, immunosuppressive, thrombolytic activities, and can be used in protein therapy. The composition and method are useful in treating inflammatory disorders, such as asthma, lung inflammation, cancer, chronic granulomatous diseases (e.g. tuberculosis, leprosy, sarcoidosis or silicosis), nephritis, amyloidosis, rheumatoid arthritis, ankylosing spondylitis, chronic bronchitis, scleroderma, lupus, appendicitis, psoriasis, pelvic inflammatory disease, orbital inflammatory disease, thrombotic disease and allergies. The present sequence represents a specifically claimed anti-inflammatory polypeptide from the present invention

Sequence 7 AA;

Query Match 100.0%; Score 41; DB 6; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7  
1 RRMKKK 7  
DB 1 RRMKKK 7

RESULT 10  
ADA61903  
ID ADA61903 standard; peptide; 7 AA.  
XX  
AC ADA61903;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE NFkB essential modulator (NEMO) binding peptide #103.  
XX  
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;  
KW antitubercular; osteopathic; antibacterial; immunosuppressive;  
KW dermatological; neuroprotective; cytostatic; nocotropic; virucide;  
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KW psoriasis; rheumatoid arthritis; osteoarthritis;  
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KW necrosis factor kappa B essential modulator.  
XX  
OS Unidentified.  
XX  
PN US2003054999-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 02-MAY-2001; 2001US-00847946.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PA (MAYM/) MAY M J.  
PA (GHOS/) GHOSH S.  
PA (FIND/) FINDERS M A.  
PA (PHIL/) PHILLIPS K.  
PA (HANN/) HANNIG G.  
XX  
PI May MJ, Ghosh S, Findels MA, Phillips K, Hannig G;  
XX  
DR WPI; 2003-596541/56.  
XX  
PT New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.  
XX  
PS Claim 11; Page 24; 37pp; English.  
XX  
CC The invention describes an anti-inflammatory compound comprising (I). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
XX  
SQ Sequence 7 AA;  
XX  
Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC ADA61896;  
XX  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE NFkB essential modulator (NEMO) binding peptide #96.  
XX  
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;  
KW antitubercular; osteopathic; antibacterial; immunosuppressive;  
KW dermatological; neuroprotective; cytostatic; nocotropic; virucide;  
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KW psoriasis; rheumatoid arthritis; osteoarthritis;  
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KW necrosis factor kappa B essential modulator.  
XX  
OS Unidentified.  
XX  
PN US2003054999-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 02-MAY-2001; 2001US-00847946.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PA (MAYM/) MAY M J.  
PA (GHOS/) GHOSH S.  
PA (FIND/) FINDERS M A.  
PA (PHIL/) PHILLIPS K.  
PA (HANN/) HANNIG G.  
XX  
PI May MJ, Ghosh S, Findels MA, Phillips K, Hannig G;  
XX  
DR WPI; 2003-596541/56.  
XX  
PT New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.  
XX  
PS Claim 11; Page 24; 37pp; English.  
XX  
CC The invention describes an anti-inflammatory compound comprising (I). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
XX  
SQ Sequence 7 AA;  
XX  
Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
ADCC22330  
ID ADCC22330 standard; peptide; 7 AA.  
XX  
AC ADCC22330;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Nuclear localisation signal motif amino acid sequence SEQ ID NO:179.

XX recombinant fusion protein; fusion protein; binding; detection;  
 KW localisation domain; binding domain;  
 KM subcellular compartment localisation.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003012068-A2.  
 XX  
 PD 13-FEB-2003.  
 XX  
 PF 01-AUG-2002; 2002WO-US024572.  
 XX  
 PR 01-AUG-2001; 2001US-0309395P.  
 PR 13-DEC-2001; 2001US-0341589P.  
 XX  
 PA (CELL-) CELLOMICS INC.  
 XX  
 PI Bright G, Premkumar DR, Chen Y;  
 XX  
 DR WPI; 2003-248174/24.  
 XX  
 PT New recombinant fusion protein comprising detection and first  
 PT localisation domains and a binding domain for the molecule of interest,  
 PT useful for detecting binding of a molecule of interest.  
 PS Claim 20; SEQ ID NO 179; 101pp; English.  
 XX  
 CC The present invention describes a recombinant fusion protein (I) for  
 CC detecting binding of a molecule of interest. (I) comprises: (a) a  
 CC detection domain; (b) a first localisation domain; and (c) a binding  
 CC domain for the molecule of interest. The detection domain, the first  
 CC localisation domain and the binding domain for the molecule of interest  
 CC constituting the recombinant fusion protein for detecting binding of a  
 CC molecule of interest are separately linked. The binding domain for the  
 CC molecule of interest is separated from the first localisation domain by 0  
 CC -20 amino acid residues. The first localisation domain and the binding  
 CC domain for the molecule of interest both do not occur in a single non-  
 CC recombinant protein with the same spacing as in the recombinant fusion  
 CC protein for detecting binding of a molecule of interest. Also described:  
 CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;  
 CC (2) a recombinant expression vector comprising the nucleic acid control  
 CC sequences operably linked to the recombinant nucleic acid molecule; (3) a  
 CC genetically engineered host cell transfected with the recombinant  
 CC expression vector; (4) a kit for detecting binding of the molecule of  
 CC interest; and (5) a method for identifying compounds that alter the  
 CC binding of the molecule of interest. The recombinant fusion protein is  
 CC useful for detecting binding of a molecule of interest. The recombinant  
 CC fusion protein eliminates the need to construct two or more chimeric  
 CC proteins and enables the monitoring of biochemical events in live, intact  
 CC or fixed cells. The present sequence is used in the exemplification of  
 CC the present invention.  
 CC  
 XX  
 SQ Sequence 7 AA;  
 XX  
 Query Match 100.0%; Score 41; DB 7; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 RRMKMKK 7  
 XX  
 AC AAY83577;  
 XX  
 AC AAY83577;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Peptide fragment of penetratin.

XX Penetratin; translocation; membrane; drug delivery; therapy; treatment;  
 KW conjugate; vector.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200029427-A2.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 11-NOV-1999; 99WO-GB003750.  
 XX  
 PR 13-NOV-1998; 98GB-00025000.  
 PR 13-NOV-1998; 98GB-00025001.  
 PR 04-FEB-1999; 99GB-00002522.  
 PR 04-FEB-1999; 99GB-00002525.  
 PR 22-JUN-1999; 99GB-00014578.  
 XX  
 PA (CYCL-) CYCLACEI LTD.  
 XX  
 PI Fischer MP, Znelev N;  
 XX  
 DR WPI; 2000-387734/33.  
 XX  
 PT New membrane translocation peptide carrier group for delivering  
 PT therapeutic agents into target cells comprises specified sequence of  
 PT amino acids.  
 XX  
 PS Example 17; Page 44; 59pp; English.  
 XX  
 CC Penetratin is a membrane translocation polypeptide and as such, active  
 CC peptide fragments of penetratin can be used to translocate conjugated  
 CC molecules across the cell membrane e.g. drugs. 13 chemical entities are  
 CC described for use in the method such as pacitaxel.  
 CC 2/succinimidopropionyl-Chetaa-RRMKKK-NH 2. The method has applications as  
 CC succinimidopropionyl-Chetaa-RRMKKK-NH 2. The method has applications as  
 CC a drug delivery system for treatment and therapy. The resulting  
 CC conjugated molecules exhibit high immunogenicity, solubility and  
 CC clearance. The penetratin peptide fragment may be truncated and or have  
 CC amino acid substitutions. See GENESBQ records AAY83520-183581  
 CC  
 XX  
 SQ Sequence 8 AA;  
 XX  
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 2 RRMKMKK 8  
 XX  
 AC AAY83541;  
 XX  
 AC AAY83541;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Peptide fragment of membrane transport vector penetratin.  
 XX  
 KW Penetratin; translocation; membrane; drug delivery; therapy; treatment;  
 KW conjugate; vector.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200029427-A2.  
 XX  
 PD 25-MAY-2000.  
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 PF 11-NOV-1999; 99WO-GB003750.  
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PR 13-NOV-1998; 98GB-00025000.
PR 13-NOV-1998; 98GB-00025001.
PR 04-FEB-1999; 99GB-00002522.
PR 04-FEB-1999; 99GB-00002525.
PR 22-JUN-1999; 99GB-00014578.
XX
XX (CYCL-) CYCLACEL LTD.
XX
XX Fischer MP, Zhelev N;
XX
XX WPI; 2000-387734/33.
XX
XX New membrane translocation peptide carrier group for delivering
XX therapeutic agents into target cells comprises specified sequence of
XX amino acids.
XX
XX Claim 5; Page 26; 59pp; English.
XX
XX Penetratin is a membrane translocation polypeptide and as such, active
XX peptide fragments of penetratin can be used to translocate conjugated
XX molecules across the cell membrane e.g. drugs. 13 chemical entities are
XX described for use in the method such as pacilitaxel.
XX 2'succinimidopropionoyl-CbetaA-RRMKWK-NH-2, and podophyllotoxin-4-
XX succinimidopropionoyl-CbetaA-RRMKWK-NH-2. The method has applications as
XX a drug delivery system for treatment and therapy. The resulting
XX conjugated molecules exhibit high immunogenicity, solubility and
XX clearance. The penetratin peptide fragment may be truncated and or have
XX amino acid substitutions. See GENSEQ records AAY83520-Y83581
XX
XX Sequence 8 AA;
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XX
XX Query Match 100.0%; Score 41; DB 3; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRMKWK 7
Db 2 RRMKWK 8
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XX ID AAY83538 standard; peptide; 8 AA.
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XX AAY83538;
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XX 29-AUG-2000 (first entry)
XX
XX Peptide fragment of membrane transport vector penetratin.
XX
XX Penetratin; translocation; membrane; drug delivery; therapy; treatment;
XX conjugate; vector.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Modified-site 1 /label= Beta-alanine
XX FT /note= "Biotinylated"
XX
XX WO200029427-A2.
XX
XX 25-MAY-2000.
XX
XX 11-NOV-1999; 99WO-GB003750.
XX
XX 13-NOV-1998; 98GB-00025000.
XX 13-NOV-1998; 98GB-00025001.
XX 04-FEB-1999; 99GB-00002522.
XX 04-FEB-1999; 99GB-00002525.
XX 22-JUN-1999; 99GB-00014578.
XX
XX (CYCL-) CYCLACEL LTD.

```

```

XX
XX Fischer MP, Zhelev N;
XX
XX WPI; 2000-387734/33.
XX
XX New membrane translocation peptide carrier group for delivering
XX therapeutic agents into target cells comprises specified sequence of
XX amino acids.
XX
XX Claim 1; Page 21; 59pp; English.
XX
XX Penetratin is a membrane translocation polypeptide and as such, active
XX peptide fragments of penetratin can be used to translocate conjugated
XX molecules across the cell membrane e.g. drugs. 13 chemical entities are
XX described for use in the method such as pacilitaxel.
XX 2'succinimidopropionoyl-CbetaA-RRMKWK-NH-2, and podophyllotoxin-4-
XX succinimidopropionoyl-CbetaA-RRMKWK-NH-2. The method has applications as
XX a drug delivery system for treatment and therapy. The resulting
XX conjugated molecules exhibit high immunogenicity, solubility and
XX clearance. The penetratin peptide fragment may be truncated and or have
XX amino acid substitutions. See GENSEQ records AAY83520-Y83581
XX
XX Sequence 8 AA;
SQ
XX
XX Query Match 100.0%; Score 41; DB 3; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRMKWK 7
Db 2 RRMKWK 8
XX
XX Search completed: August 11, 2004, 14:00:37
XX Job time : 54 secs

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Wed Aug 11 15:42:13 2004

us-09-854-204-2.open.rapb

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:01:53 ; Search time 42 Seconds  
(without alignments)  
52.321 Million cell updates/sec

Title: US-09-854-204-2

Perfect score: 41

Sequence: 1 RRMKMKK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1292805 segs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	41	100.0	7 9 US-09-854-204-2	Sequence 2, Appl1
2	41	100.0	7 9 US-09-854-204-2	Sequence 6, Appl1
3	41	100.0	7 10 US-09-847-946A-123	Sequence 123, App
4	41	100.0	7 10 US-09-847-946A-130	Sequence 130, App
5	41	100.0	7 12 US-10-144-549-4	Sequence 4, Appl1
6	41	100.0	7 14 US-10-229-915-11	Sequence 11, Appl1
7	41	100.0	7 14 US-10-211-088-179	Sequence 179, App
8	41	100.0	7 14 US-10-210-660-2	Sequence 2, Appl1
9	41	100.0	7 14 US-10-210-660-26	Sequence 26, Appl1
10	41	100.0	7 14 US-10-315-820-22	Sequence 22, Appl1
11	41	100.0	8 9 US-09-854-204-6	Sequence 6, Appl1
12	41	100.0	8 9 US-09-854-204-54	Sequence 54, Appl1
13	41	100.0	8 14 US-10-229-915-10	Sequence 10, Appl1
14	41	100.0	8 14 US-10-210-660-3	Sequence 3, Appl1
15	41	100.0	8 14 US-10-210-660-24	Sequence 24, Appl1

16	41	100.0	9 9 US-09-854-204-7	Sequence 7, Appl1
17	41	100.0	9 9 US-09-854-204-53	Sequence 53, Appl1
18	41	100.0	9 9 US-09-854-204-61	Sequence 61, Appl1
19	41	100.0	9 9 US-09-854-204-62	Sequence 62, Appl1
20	41	100.0	9 14 US-10-229-915-9	Sequence 9, Appl1
21	41	100.0	9 14 US-10-210-660-4	Sequence 4, Appl1
22	41	100.0	9 14 US-10-210-660-19	Sequence 19, Appl1
23	41	100.0	9 14 US-10-210-660-21	Sequence 21, Appl1
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25	41	100.0	10 9 US-09-854-204-52	Sequence 52, Appl1
26	41	100.0	10 14 US-10-229-915-8	Sequence 8, Appl1
27	41	100.0	10 14 US-10-210-660-5	Sequence 5, Appl1
28	41	100.0	11 9 US-09-854-204-51	Sequence 51, Appl1
29	41	100.0	11 14 US-10-229-915-7	Sequence 7, Appl1
30	41	100.0	12 9 US-09-854-204-50	Sequence 50, Appl1
31	41	100.0	12 10 US-09-847-946A-43	Sequence 43, Appl1
32	41	100.0	12 14 US-10-229-915-6	Sequence 6, Appl1
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34	41	100.0	13 10 US-09-847-946A-143	Sequence 143, App
35	41	100.0	13 10 US-09-847-946A-144	Sequence 144, App
36	41	100.0	13 14 US-10-097-175-102	Sequence 102, App
37	41	100.0	13 14 US-10-229-915-5	Sequence 5, Appl1
38	41	100.0	14 9 US-09-854-204-48	Sequence 48, Appl1
39	41	100.0	14 14 US-10-229-915-4	Sequence 4, Appl1
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41	41	100.0	15 10 US-09-865-291-18	Sequence 18, Appl1
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44	41	100.0	16 9 US-09-214-371-43	Sequence 38, Appl1
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#### ALIGNMENTS

RESULT 1

US-09-854-204-2

Sequence 2, Application US/09854204

Patent No. US20020098236A1

GENERAL INFORMATION:

APPLICANT: Fischer, Peter Martin

APPLICANT: Zhelev, Nikolai

TITLE OF INVENTION: Transport Vectors

FILE REFERENCE: CCI-010

CURRENT APPLICATION NUMBER: US/09/854, 204

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 09/438, 460

PRIOR FILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: GB 9825000.4

PRIOR FILING DATE: 1998-11-13

PRIOR APPLICATION NUMBER: GB 9825001.2

PRIOR FILING DATE: 1998-11-13

PRIOR APPLICATION NUMBER: GB 9902525.6

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: GB 9902522.3

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: GB 9914578.1

PRIOR FILING DATE: 1999-06-22

PRIOR APPLICATION NUMBER: PCT/GB99/03750

PRIOR FILING DATE: 1999-11-11

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

NAME/KEY: MOD\_RES

LOCATION: (7)

OTHER INFORMATION: AMIDATION; the carboxyl terminal lysine residue may have its carboxyl group converted into an

OTHER INFORMATION: carboxamide group.  
US-09-854-204-2

Query Match 100.0%; Score 41; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
Db 1 RRMKWK 7

RESULT 2  
US-09-785-802A-6  
Sequence 6, Application US/09785802A  
Patent No. US20020151004A1  
GENERAL INFORMATION:  
APPLICANT: Craig, Roger  
TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME  
FILE REFERENCE: 11067/2035  
CURRENT APPLICATION NUMBER: US/09/785,802A  
CURRENT FILING DATE: 2001-02-16  
PRIOR APPLICATION NUMBER: US 09/748,06  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/748,789  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-785-802A-6

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Db 1 RRMKWK 7

RESULT 3  
US-09-847-946A-123  
Sequence 123, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 123  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:membrane  
US-09-847-946A-123

Query Match 100.0%; Score 41; DB 10; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
Db 1 RRMKWK 7

RESULT 4  
US-09-847-946A-130  
Sequence 130, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 130  
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ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:membrane  
US-09-847-946A-130

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Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
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RESULT 5  
US-10-144-549-4  
Sequence 4, Application US/10144549  
Publication No. US20030211590A1  
GENERAL INFORMATION:  
APPLICANT: Geneshuttle Biopharm, Inc.  
APPLICANT: Hwu, Paul L.  
TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR  
FILE REFERENCE: MBH 02-140  
CURRENT APPLICATION NUMBER: US/10/144,549  
CURRENT FILING DATE: 2002-05-13  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-10-144-549-4

Query Match 100.0%; Score 41; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
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QY 1 RRMKWK 7  
Db 1 RRMKWK 7

## RESULT 6

US-10-229-915-11  
; Sequence 11, Application US/10229915  
; Publication No. US20030083262A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazarus, Douglas  
; APPLICANT: Hanig, Gerhard  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY  
; FILE REFERENCE: PPI-127  
; CURRENT APPLICATION NUMBER: US/10/229,915  
; PRIOR FILING DATE: 2002-08-27  
; PRIOR APPLICATION NUMBER: US 60/316,328  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
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; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: anti-inflammatory compound  
US-10-229-915-11

## Query Match

100.0%; Score 41; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
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DB 1 RRMKKKK 7

## RESULT 7

US-10-211-088-179  
; Sequence 179, Application US/10211088  
; Publication No. US20030104479A1  
; GENERAL INFORMATION:  
; APPLICANT: Bright, Gary R.  
; APPLICANT: Premkumar, D. David  
; APPLICANT: Chen, Yih-Tai  
; TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins And Assays For Molecular Bi  
; FILE REFERENCE: 01-1022-US  
; CURRENT APPLICATION NUMBER: US/10/211,088  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/309,395  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/341,589  
; PRIOR FILING DATE: 2001-12-13  
; NUMBER OF SEQ ID NOS: 366  
; SOFTWARE: PatentIn version 3.1  
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; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Nuclear localization signal  
US-10-211-088-179

## Query Match

100.0%; Score 41; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 RRMKKKK 7

## RESULT 8

US-10-210-660-2  
; Sequence 2, Application US/10210660  
; Publication No. US20030119735A1

## GENERAL INFORMATION:

; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/10/210,660  
; CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US/09/346,847  
; PRIOR FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-210-660-2

## Query Match

100.0%; Score 41; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
| | | | |  
DB 1 RRMKKKK 7

## RESULT 9

US-10-210-660-26  
; Sequence 26, Application US/10210660  
; Publication No. US20030119735A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/10/210,660  
; CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US/09/346,847  
; PRIOR FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (7)\_"RES"  
; OTHER INFORMATION: AMIDATION  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-210-660-26

## Query Match

100.0%; Score 41; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
| | | | |  
DB 1 RRMKKKK 7

## RESULT 10

US-10-315-920-22  
; Sequence 22, Application US/10315920

```
Publication No. US20030175809A1
GENERAL INFORMATION:
APPLICANT: Fradkov, Arcady Fedorovich
APPLICANT: Terzikikh, Alexey
TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
FILE REFERENCE: CION-077CIP
CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 60/211,607
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: PCT/US01/19097
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nuclear localization signal
US-10-315-920-22

Query Match
Best Local Similarity 100.0%; Score 41; DB 14; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
Db 1 RRMKWK 7

RESULT 11
US-09-854-204-6
Sequence 6, Application US/09854204
Patent No. US20020098236A1
GENERAL INFORMATION:
APPLICANT: Fischer, Peter Martin
APPLICANT: Zhelev, Nikolai
TITLE OF INVENTION: Transport Vectors
FILE REFERENCE: CCI-010
CURRENT APPLICATION NUMBER: US/09/854,204
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/438,460
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: GB 9825000.4
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: GB 9825001.2
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: GB 9902525.6
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: GB 9902522.3
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: GB 9914578.1
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: PCT/GB99/03750
PRIOR FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-854-204-6

Query Match
Best Local Similarity 100.0%; Score 41; DB 9; Length 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
Db 1 RRMKWK 7
```

```
Db 2 RRMKWK 8

RESULT 12
US-09-854-204-54
Sequence 54, Application US/09854204
Patent No. US20020098236A1
GENERAL INFORMATION:
APPLICANT: Fischer, Peter Martin
APPLICANT: Zhelev, Nikolai
TITLE OF INVENTION: Transport Vectors
FILE REFERENCE: CCI-010
CURRENT APPLICATION NUMBER: US/09/854,204
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/438,460
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: GB 9825000.4
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: GB 9825001.2
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: GB 9902525.6
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: GB 9902522.3
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: GB 9914578.1
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: PCT/GB99/03750
PRIOR FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 54
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Data
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: AMIDATION
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-854-204-54

Query Match
Best Local Similarity 100.0%; Score 41; DB 9; Length 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
Db 2 RRMKWK 8

RESULT 13
US-10-229-915-10
Sequence 10, Application US/10229915
Patent No. US20030083262A1
GENERAL INFORMATION:
APPLICANT: Lazarus, Douglas
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
FILE REFERENCE: PFI-127
CURRENT APPLICATION NUMBER: US/10/229,915
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: US 60/316,328
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 8
```

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: anti-inflammatory compound  
US-10-229-915-10

Query Match 100.0%; Score 41; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
Db 2 RRMKWK 8

RESULT 14  
US-10-210-660-3  
Sequence 3, Application US/10210660  
Publication No. US20030119735A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/10/210,660  
CURRENT FILING DATE: 2002-07-31  
PRIOR APPLICATION NUMBER: US/09/346,847  
PRIOR FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-210-660-3

Query Match 100.0%; Score 41; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
Db 2 RRMKWK 8

RESULT 15  
US-10-210-660-24

Sequence 24, Application US/10210660  
Publication No. US20030119735A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/10/210,660  
CURRENT FILING DATE: 2002-07-31  
PRIOR APPLICATION NUMBER: US/09/346,847  
PRIOR FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES

LOCATION: (1)  
OTHER INFORMATION: bala  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (8)  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
FEATURE:  
OTHER INFORMATION: AMIDATION  
US-10-210-660-24

Query Match 100.0%; Score 41; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
Db 2 RRMKWK 8

Search completed: August 11, 2004, 14:07:20  
Job time : 42 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2004, 13:59:42 ; Search time 18 Seconds  
(without alignments)  
20.077 Million cell updates/sec

Title: US-09-854-204-2  
Perfect score: 41  
Sequence: 1 RRMKKK 7

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
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6: /cgn2\_6/ptodata/2/1aa/6D.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	7	US-09-346-847-2	Sequence 2, Appli
2	41	100.0	7	US-09-346-847-26	Sequence 26, Appli
3	41	100.0	8	US-09-346-847-3	Sequence 3, Appli
4	41	100.0	8	US-09-346-847-24	Sequence 24, Appli
5	41	100.0	9	US-09-346-847-4	Sequence 4, Appli
6	41	100.0	9	US-09-346-847-19	Sequence 19, Appli
7	41	100.0	9	US-09-346-847-21	Sequence 21, Appli
8	41	100.0	10	US-09-346-847-5	Sequence 5, Appli
9	41	100.0	16	US-08-928-958-7	Sequence 7, Appli
10	41	100.0	16	US-08-810-540-3	Sequence 3, Appli
11	41	100.0	16	US-08-810-540-6	Sequence 6, Appli
12	41	100.0	16	US-09-072-429-7	Sequence 7, Appli
13	41	100.0	16	US-08-964-302A-6	Sequence 6, Appli
14	41	100.0	16	US-09-116-294-4	Sequence 4, Appli
15	41	100.0	16	US-08-964-614A-4	Sequence 4, Appli
16	41	100.0	16	US-08-849-486-1	Sequence 1, Appli
17	41	100.0	16	US-08-849-486-4	Sequence 4, Appli
18	41	100.0	16	US-08-849-486-5	Sequence 5, Appli
19	41	100.0	16	US-09-208-966-1	Sequence 1, Appli
20	41	100.0	16	US-09-208-966-54	Sequence 54, Appli
21	41	100.0	16	US-09-308-935-8	Sequence 8, Appli
22	41	100.0	16	US-09-441-416A-6	Sequence 6, Appli
23	41	100.0	16	US-09-296-089-33	Sequence 33, Appli
24	41	100.0	16	US-09-419-826-35	Sequence 35, Appli
25	41	100.0	16	US-09-466-772-7	Sequence 7, Appli
26	41	100.0	16	US-09-302-305C-10	Sequence 10, Appli
27	41	100.0	16	US-09-402-929-7	Sequence 7, Appli

28	41	100.0	16	US-09-346-847-1	Sequence 1, Appli
29	41	100.0	16	US-09-346-847-25	Sequence 25, Appli
30	41	100.0	16	US-09-057-363C-47	Sequence 47, Appli
31	41	100.0	16	US-09-043-560B-3	Sequence 3, Appli
32	41	100.0	16	US-09-648-400A-29	Sequence 29, Appli
33	41	100.0	16	US-09-227-652B-4	Sequence 4, Appli
34	41	100.0	16	US-09-780-070-38	Sequence 38, Appli
35	41	100.0	16	US-08-610-220B-9	Sequence 9, Appli
36	41	100.0	16	US-09-775-052A-1	Sequence 1, Appli
37	41	100.0	16	US-09-775-052A-34	Sequence 54, Appli
38	41	100.0	16	US-09-155-165-22	Sequence 22, Appli
39	41	100.0	16	US-09-792-480-29	Sequence 29, Appli
40	41	100.0	16	US-09-792-480-30	Sequence 30, Appli
41	41	100.0	16	US-09-551-976-33	Sequence 33, Appli
42	41	100.0	16	US-09-265-107-47	Sequence 47, Appli
43	41	100.0	17	US-09-346-847-17	Sequence 17, Appli
44	41	100.0	17	US-09-346-847-20	Sequence 20, Appli
45	41	100.0	17	US-09-346-847-22	Sequence 22, Appli

## ALIGNMENTS

RESULT 1  
US-09-346-847-2  
Sequence 2, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-346-847-2

Query Match  
Best Local Similarity 100.0%; Score 41; DB 4; Length 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7  
Db 1 RRMKKK 7

RESULT 2  
US-09-346-847-26  
Sequence 26, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 7

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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)
OTHER INFORMATION: AMIDATION
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-346-847-26
```

```
Query Match
Best Local Similarity 100.0%; Score 41; DB 4; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RRMKWK 7
DB 1 RRMKWK 7
```

```
RESULT 3
US-09-346-847-3
Sequence 3, Application US/09346847
Patent No. 6472507
GENERAL INFORMATION:
APPLICANT: Fischer, M. Peter
TITLE OF INVENTION: Delivery System
FILE REFERENCE: CCI-009
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: GB 9814527
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-346-847-3
```

```
Query Match
Best Local Similarity 100.0%; Score 41; DB 4; Length 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RRMKWK 7
DB 2 RRMKWK 8
```

```
RESULT 4
US-09-346-847-24
Sequence 24, Application US/09346847
Patent No. 6472507
GENERAL INFORMATION:
APPLICANT: Fischer, M. Peter
TITLE OF INVENTION: Delivery System
FILE REFERENCE: CCI-009
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: GB 9814527
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
```

```
LOCATION: (1)
OTHER INFORMATION: bala
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: AMIDATION
US-09-346-847-24
```

```
Query Match
Best Local Similarity 100.0%; Score 41; DB 4; Length 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RRMKWK 7
DB 2 RRMKWK 8
```

```
RESULT 5
US-09-346-847-4
Sequence 4, Application US/09346847
Patent No. 6472507
GENERAL INFORMATION:
APPLICANT: Fischer, M. Peter
TITLE OF INVENTION: Delivery System
FILE REFERENCE: CCI-009
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: GB 9814527
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-346-847-4
```

```
Query Match
Best Local Similarity 100.0%; Score 41; DB 4; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RRMKWK 7
DB 3 RRMKWK 9
```

```
RESULT 6
US-09-346-847-19
Sequence 19, Application US/09346847
Patent No. 6472507
GENERAL INFORMATION:
APPLICANT: Fischer, M. Peter
TITLE OF INVENTION: Delivery System
FILE REFERENCE: CCI-009
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: GB 9814527
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (2)
```



```
OTHER INFORMATION: Data
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
NAME/KEY: MOD_RES
LOCATION: (9)
OTHER INFORMATION: AMIDATION
US-09-346-847-19

Query Match
Best Local Similarity 100.0%; Score 41; DB 4; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
    |||||
Db 3 RRMKWK 9

RESULT 7
US-09-346-847-21
Sequence 21, Application US/09346847
Patent No. 6472507
GENERAL INFORMATION:
APPLICANT: Fischer, M. Peter
APPLICANT: Wang, Shudong
TITLE OF INVENTION: Delivery System
FILE REFERENCE: CCI-009
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: GB 9814527
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 9
TYPE: PRP
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
NAME/KEY: MOD_RES
LOCATION: (9)
OTHER INFORMATION: AMIDATION
US-09-346-847-21

Query Match
Best Local Similarity 100.0%; Score 41; DB 4; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
    |||||
Db 2 RRMKWK 8

RESULT 8
US-09-346-847-5
Sequence 5, Application US/09346847
Patent No. 6472507
GENERAL INFORMATION:
APPLICANT: Fischer, M. Peter
APPLICANT: Wang, Shudong
TITLE OF INVENTION: Delivery System
FILE REFERENCE: CCI-009
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: GB 9814527
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 10
TYPE: PRP
ORGANISM: Artificial Sequence
FEATURE:
```

```
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-346-847-5

Query Match
Best Local Similarity 100.0%; Score 41; DB 4; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
    |||||
Db 4 RRMKWK 10

RESULT 9
US-08-928-958-7
Sequence 7, Application US/08928958
Patent No. 5877282
GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
APPLICANT: CLEVELAND, JEFFREY S.
APPLICANT: BLAKE, JAMES
APPLICANT: HARRAR, OMAR K.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
TITLE OF INVENTION: TRANSLATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-928-958-7

Query Match
Best Local Similarity 100.0%; Score 41; DB 2; Length 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
    |||||
Db 10 RRMKWK 16

RESULT 10
US-08-810-540-3
Sequence 3, Application US/08810540
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Patent No. 5929042  
GENERAL INFORMATION:  
APPLICANT: Troy, Carol M.  
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL  
GROWTH  
TITLE OF INVENTION: DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham, LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,540  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-810-540-3

Query Match 100.0%; Score 41; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7  
DB 10 RRMKKK 16

RESULT 11  
US-08-810-540-6  
Sequence 6, Application US/08810540  
Patent No. 5929042  
GENERAL INFORMATION:  
APPLICANT: Troy, Carol M.  
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL  
GROWTH  
TITLE OF INVENTION: DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham, LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,540  
FILING DATE: 03-MAR-1997

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-810-540-6

Query Match 100.0%; Score 41; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7  
DB 10 RRMKKK 16

RESULT 12  
US-09-072-429-7  
Sequence 7, Application US/09072429  
Patent No. 5962415  
GENERAL INFORMATION:  
APPLICANT: Nadler, Steven G.  
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE  
INHIBITOR OF NUCLEAR PROTEIN TRANSLLOCATION AND AN  
IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: P.O. Box 4000  
CITY: Princeton  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08543-4000  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/072,429  
FILING DATE: 04-MAY-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Klein, Christopher A.  
REGISTRATION NUMBER: 34,363  
REFERENCE/DOCKET NUMBER: 090141b  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 252-3714  
TELEFAX: (609) 252-4526  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-072-429-7

Query Match 100.0%; Score 41; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7

Db 10 RRMKWK 16

## RESULT 13

US-08-964-302A-6  
Sequence 6, Application US/08964302A  
Patent No. 6015787  
GENERAL INFORMATION:  
APPLICANT: Potter, David A.  
APPLICANT: Skolnik, Paul R.  
TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF CALPAIN  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,302A  
FILING DATE: 04-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielehn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 00398/126001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-964-302A-6

Query Match Best Local Similarity 100.0%; Score 41; DB 3; Length 16;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
Db 10 RRMKWK 16

## RESULT 14

US-09-116-294-4  
Sequence 4, Application US/09116294  
Patent No. 6025140  
GENERAL INFORMATION:  
APPLICANT: Langel, Udo  
APPLICANT: Bartfai, Tamás  
APPLICANT: Pösga, Margus  
APPLICANT: Valkna, Andres  
APPLICANT: Saar, Kulliki  
TITLE OF INVENTION: Conjugated Constructs of Peptides and  
TITLE OF INVENTION: Nucleic Acid Analogs, and Their Transport Across Membranes  
FILE REFERENCE: 4394  
CURRENT APPLICATION NUMBER: US/09/116,294  
CURRENT FILING DATE: 1998-07-16  
EARLIER APPLICATION NUMBER: 60/052,678  
EARLIER FILING DATE: 1997-07-24  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4  
LENGTH: 16  
TYPE: PRT  
ORGANISM: drosophila  
US-09-116-294-4

Query Match Best Local Similarity 100.0%; Score 41; DB 3; Length 16;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
Db 10 RRMKWK 16

## RESULT 15

US-08-964-614A-4  
Sequence 4, Application US/08964614A  
Patent No. 6057104  
GENERAL INFORMATION:  
APPLICANT: Hasely, Paul  
TITLE OF INVENTION: DISRUPTION OF THE MAMMALIAN  
TITLE OF INVENTION: Rad51 PROTEIN AND DISRUPTION OF PROTEINS THAT ASSOCIATE  
TITLE OF INVENTION: WITH MAMMALIAN Rad51 FOR HINDERING CELL PROLIFERATION  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,614A  
FILING DATE: 05-NOV-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/758,280  
FILING DATE: 05-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8535-0019-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-964-614A-4

Query Match Best Local Similarity 100.0%; Score 41; DB 3; Length 16;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
Db 10 RRMKWK 16

Search completed: August 11, 2004, 14:02:44  
Job time: 18 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:06:34 ; Search time 16 Seconds  
(without alignments)  
42.084 Million cell updates/sec

Title: US-09-854-204-2  
Perfect score: 41  
Sequence: 1 RRMKWK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR78:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	17	41.5	7	2 S33244	neuromodulatory pe
2	17	41.5	7	2 S33246	neuromodulatory pe
3	16	39.0	3	3 F37196	bradykinin-potent
4	16	39.0	3	2 UH0253	gut pentapeptide
5	16	39.0	5	2 G37196	bradykinin-potent
6	16	39.0	7	2 PN0649	pullulanase (EC 3.
7	15	36.6	5	2 A60803	neuropeptide - sea
8	15	36.6	6	2 I49424	cytotoxic T-lympho
9	14	34.1	7	2 S33245	neuromodulatory pe
10	14	31.7	6	4 I79564	hypothetical TGL3
11	12	29.3	4	2 I40870	phospholipase C (E
12	12	29.3	5	2 PT0308	ig heavy chain CRD
13	12	29.3	6	2 S66195	alcohol dehydrogen
14	12	29.3	6	2 S11024	hydrogensulfite re
15	12	29.3	6	2 S11556	hydrogensulfite re
16	12	29.3	6	2 A31263	dihydrofolate redu
17	12	29.3	6	2 B31263	dihydrofolate redu
18	12	29.3	6	2 B3640	ribosomal protein
19	12	29.3	7	2 S19630	hypothetical pepti
20	12	29.3	7	4 I55382	hypothetical pepti
21	11	26.8	4	2 A34626	RPCR-related neuro
22	11	26.8	4	2 B53284	T-cell receptor be
23	11	26.8	4	2 PT0661	T-cell receptor be
24	11	26.8	5	2 A32516	cholecystokinin-5
25	11	26.8	5	2 PT0281	ig heavy chain CRD
26	11	26.8	5	2 PT0729	T-cell receptor be
27	11	26.8	5	2 PT0560	T-cell receptor be
28	11	26.8	6	2 B34835	dnma protein - pse
29	11	26.8	6	2 A61068	locustactin - mlg

30	11	26.8	6	2 PT0629	T-cell receptor be
31	11	26.8	6	2 PT0532	T-cell receptor be
32	11	26.8	6	2 PT0519	T-cell receptor be
33	11	26.8	6	2 PT0637	T-cell receptor be
34	11	26.8	6	2 PT0641	T-cell receptor be
35	11	26.8	6	2 PT0726	T-cell receptor be
36	11	26.8	6	2 F41946	T-cell receptor ga
37	11	26.8	6	2 PD0028	pev-kinin 2 - pena
38	11	26.8	7	2 S21230	dermorphin (Trp-4,
39	11	26.8	7	2 AS8512	venom heptapeptide
40	11	26.8	7	2 A61081	cryptophyllin, bas
41	11	26.8	7	2 S57274	triacylglycerol 11
42	11	26.8	7	2 S09652	hypothetical prote
43	11	26.8	7	2 PQ0727	H2 class I protein
44	11	26.8	7	2 E48394	glycoprotein compo
45	11	26.8	7	2 B33541	hypothetical prote

## ALIGNMENTS

RESULT 1  
S33244 neuromodulatory peptide Wamide-1 - giant African snail  
C/Species: Achatina fulica (giant African snail)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C/Accession: S33244  
R/Minakata, H.; Ikeda, T.; Munoe, Y.; Kobayashi, M.; Nomoto, K.  
FEB5 Lett. 323: 104-108, 1993  
A/Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t  
A/Reference number: S33244; MUID:93265912; PMID:8495720  
A/Accession: S33244  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <MIN>

Query Match 41.5%; Score 17; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 WKX 7  
DB 1 WKX 3

RESULT 2  
S33246 neuromodulatory peptide Wamide-3 - giant African snail  
C/Species: Achatina fulica (giant African snail)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C/Accession: S33246  
R/Minakata, H.; Ikeda, T.; Munoe, Y.; Kobayashi, M.; Nomoto, K.  
FEB5 Lett. 323: 104-108, 1993  
A/Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t  
A/Reference number: S33244; MUID:93265912; PMID:8495720  
A/Accession: S33246  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <MIN>

Query Match 41.5%; Score 17; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 WKX 7  
DB 1 WKX 3

RESULT 3  
F37196 bradykinin-potentiating peptide 6 - island jararaca  
C/Species: Bothrops insularis (island jararaca)

C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C/Accession: F37196  
R/Cintr, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990  
A/Title: Primary structure and biological activity of bradykinin potentiating peptides  
A/Reference number: A37196; PMID:90351557; PMID:2386615  
A/Accession: F37196

A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-3 <CIN>  
C/Keywords: pyroglutamic acid  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match  
Best Local Similarity 39.0%; Score 16; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KW 5  
DB 2 KW 3

RESULT 4  
JH0253

gut pentapeptide - Japanese eel  
C/Species: Anguilla japonica (Japanese eel)  
C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C/Accession: JH0253

R/Iesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.

Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A/Title: Structure and function of a pentapeptide isolated from the gut of the eel.

A/Reference number: JH0253; PMID:92062113; PMID:1953755  
A/Accession: JH0253

A/Molecule type: protein  
A/Residues: 1-5 <UHS>  
A/Experimental source: gut  
A/Comment: This peptide increased basal tone of the circular muscle of the esophagogastric  
and of the circular muscle of the gastro-intestinal junction.

Query Match  
Best Local Similarity 39.0%; Score 16; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 WKX 7  
DB 3 WKX 5

RESULT 5  
G37196

bradykinin-potentiating peptide 7 - island jararaca  
C/Species: Bothrops insularis (island jararaca)

C/Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994  
C/Accession: G37196

R/Cintr, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A/Title: Primary structure and biological activity of bradykinin potentiating peptides  
A/Reference number: A37196; PMID:90351557; PMID:2386615  
A/Accession: G37196

A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-5 <CIN>  
C/Keywords: pyroglutamic acid  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match  
Best Local Similarity 39.0%; Score 16; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KW 5  
DB 2 KW 3

RESULT 6

PN0649  
pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)

C/Species: Bacillus sp.

C/Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 03-Jun-2002  
C/Accession: PN0649

R/Kim, C.H.; Choi, H.I.; Lee, D.S.

Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993  
A/Title: Purification and biochemical properties of an alkaline pullulanase from alkalop

A/Reference number: PN0649; PMID:94080025; PMID:7764261  
A/Accession: PN0649

A/Molecule type: protein  
A/Residues: 1-7 <KIM>

C/Comment: This enzyme is used together with glucosylase to improve the efficiency of st

C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match  
Best Local Similarity 39.0%; Score 16; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 MKW 5  
DB 4 MSW 6

RESULT 7

neuropeptide - sea anemone (Anthopleura elegantissima)

C/Species: Anthopleura elegantissima

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: A60803

R/Graff, D.; Grimmelikhuijzen, C.J.P.

Brain Res. 442, 354-358, 1988

A/Title: Isolation of <Glu-Ser-Ileu-Arg-Tyr-NH-2> a novel neuropeptide from sea anemones.

A/Reference number: A60803; PMID:68222764; PMID:2897223  
A/Accession: A60803

A/Molecule type: protein  
A/Residues: 1-5 <GRA>

C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match  
Best Local Similarity 36.6%; Score 15; DB 2; Length 5;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MKW 5  
DB 3 LKW 5

RESULT 8

149424  
cytochrome T-lymphocyte proteinase 3 (EC 3.4.21.-) - western wild mouse (fragment)

C/Species: Mns sylvaticus (western wild mouse)

C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C/Accession: 149424

R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.

Mamm. Genome 5, 349-355, 1994

A/Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A/Reference number: 148934; PMID:94319082; PMID:8043949  
A/Accession: 149424

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
A/Residues: 1-6 <RES>

A/Cross-references: EMBL:U05745; NID:9497084; PIDN:AAB60481.1; PID:9642831  
C/Keywords: hydrolase; serine proteinase

Query Match  
Best Local Similarity 36.6%; Score 15; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RMK 4  
1 RMK 4  
DB

## RESULT 9

S33245  
neuromodulatory peptide Wamide-2 - giant African snail  
C:Species: Achatina fulica (giant African snail)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C:Accession: S33245  
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.  
FEBS Lett. 333, 104-108, 1993  
A>Title: Wamide-1, -2 and -3; novel neuromodulatory peptides isolated from ganglia of A.  
A:Reference number: S33244; MUID:93265912; PMID:8495720  
A:Accession: S33245  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <MIN>

Query Match 34.1%; Score 14; DB 2; Length 7;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 WK 7  
1 RMK 3  
DB

## RESULT 10

I79564  
hypothetical TCJ3 protein (mitrtranslated) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 28-Jan-2000 #sequence\_revision 28-Jan-2000 #text\_change 28-Jan-2000  
C:Accession: I79564  
R:Zutter, M.; Hockett, R.D.; Roberts, C.W.; McGuire, E.A.; Bloomstone, J.; Morton, C.C.;  
Proc Natl. Acad. Sci. U.S.A. 87, 3161-3165, 1990  
A>Title: The t(10;14)(q24;q11) of T-cell acute lymphoblastic leukemia juxtaposes the del  
A:Reference number: I59162; MUID:90222189; PMID:2326274  
A:Accession: I79564  
A>Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <ZUT>  
A:Cross-references: GB:M33602; NID:9339907; PIDN:AA66449.1; PID:9807656  
C:Comment: This is the hypothetical translation of a sequence translated in an incorrect

Query Match 31.7%; Score 13; DB 4; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 KM 5  
1 RMK 2  
DB

## RESULT 11

I40870  
phospholipase C (EC 3.1.4.3) - Clostridium perfringens (fragment)  
C:Species: Clostridium perfringens  
C>Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 21-Jul-2000  
C:Accession: I40870  
R:Toyonaga, T.; Matsushita, O.; Katayama, S.; Minami, J.; Okabe, A.  
Microbiol. Immunol. 36, 603-613, 1992  
A>Title: Role of the upstream region containing an intrinsic DNA curvature in the negati  
A:Reference number: I40870; MUID:92396045; PMID:1522810  
A:Accession: I40870  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-4 <RES>  
A:Cross-references: EMBL:X62825; NID:940622; PIDN:CAA44636.1; PID:94377417  
C:Genetics:  
A:Gene: plc

C:Keywords: phosphoric diester hydrolase  
Query Match 29.3%; Score 12; DB 2; Length 4;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 MKK 6  
1 MKK 4  
DB

## RESULT 12

PT0308  
I9 heavy chain CRD3 region (clone 6-88) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0308  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A:Reference number: PT0222; MUID:9108337; PMID:1899102  
A:Accession: PT0308  
A:Molecule type: DNA  
A:Residues: 1-5 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.3%; Score 12; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 WK 6  
2 WK 3  
DB

## RESULT 13

S66195  
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragme  
C:Species: Gadus sp. (cod)  
C>Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 12-Jun-1998  
C:Accession: S66195  
R:Hjeltnes, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;  
FEBS Lett. 367, 237-240, 1995  
A>Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. N  
nzyme.  
A:Reference number: S66191; MUID:95331382; PMID:7607314

Query Match 29.3%; Score 12; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 WK 6  
5 WK 6  
DB

## RESULT 14

S11024  
N-hydroxyethylamine reductase (EC 1.8.99.3) chain 1 - Desulfovibrio thermophilus (fragment)  
N:Alternate names: bisulfite reductase; desulfotetracycline  
C:Species: Desulfovibrio thermophilus  
C>Date: 19-Mar-1997 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
C:Accession: S11024  
R:Paugue, G.; Lino, A.R.; Czochowski, M.; Kang, L.; DeVartanian, D.V.; Moura, J.J.G.; I  
Biochim. Biophys. Acta 1040, 112-118, 1990  
A>Title: Purification and characterization of bisulfite reductase (desulfotetracycline) from  
A:Reference number: S11024; MUID:90335276; PMID:2165817

A;Accession: S11024  
 A;Molecule type: protein  
 A;Residues: 1-6 <FAU>  
 C;Keywords: oxidoreductase

Query Match 29.3%; Score 12; DB 2; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MKWK 6  
 :|:|  
 Db 3 VKFK 6

## RESULT 15

S11556  
 hydrogensulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment)  
 N;Alternate names: bisulfite reductase; desulfofuscidin  
 C;Species: Desulfovibrio thermophilus  
 C;Date: 19-Mar-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
 C;Accession: S11556  
 R;Paque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DeVartanian, D.V.; Moura, J.C.G.; I  
 Biochim. Biophys. Acta 1040, 112-118, 1990  
 A;Title: Purification and characterization of bisulfite reductase (desulfofuscidin) from  
 A;Reference number: S11024; MWID:90335276; PMID:2165817  
 A;Accession: S11556  
 A;Molecule type: protein  
 A;Residues: 1-6 <FAU>  
 C;Keywords: oxidoreductase

Query Match 29.3%; Score 12; DB 2; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KWK 6  
 :|:|  
 Db 4 KYK 6

Search completed: August 11, 2004, 14:09:58  
 Job time : 17 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:02:48 ; Search time 13 Seconds

(without alignments)  
28.038 Million cell updates/sec

Title: US-09-854-204-2

Perfect score: 41  
Sequence: 1 RRMKMK 7

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	41.5	7	1	WMW2_ACHFU
2	17	41.5	7	1	WMW3_ACHFU
3	16	39.0	5	1	BPP7_BOTIN
4	14	34.1	7	1	WMW1_ACHFU
5	13	31.7	5	1	UF01_MOUSE
6	12	29.3	7	1	Y151_LITRU
7	11	26.8	4	1	OCB3_OCTMI
8	11	26.8	6	1	E101_LITRU
9	11	26.8	6	1	LOK1_LOCM1
10	11	26.8	7	1	BRHP_CONIM
11	11	26.8	7	1	TPRY_PACDA
12	10	24.4	6	1	VP19_HSVIK
13	8	19.5	4	1	FAR4_HIRME
14	8	19.5	4	1	PMR7_YACNI
15	8	19.5	7	1	FAR3_HABCO
16	8	19.5	7	1	FAR3_PANRE
17	8	19.5	7	1	FARS_HIRME
18	8	19.5	7	1	FARB_CALVO
19	7	17.1	5	1	FARP_ARTTR
20	7	17.1	6	1	ACPH_RABIT
21	7	17.1	6	1	OVN_LEPDE
22	7	17.1	7	1	ALU7_CYDPO
23	7	17.1	7	1	CARP_MYTED
24	7	17.1	7	1	HY7_FIG
25	6	14.6	3	1	LUXE_VIBRI
26	6	14.6	4	1	FRFA_ANTEL
27	6	14.6	4	1	FIRI_ANTEL
28	6	14.6	6	1	ASP2_LACSN
29	5	12.2	3	1	GRWM_HUMAN
30	5	12.2	4	1	DCML_PSECH
31	5	12.2	4	1	DCMS_PSECH
32	5	12.2	4	1	FAR3_HIRME
33	5	12.2	4	1	FLRF_HIRME

34	5	12.2	4	1	FLRN_ANTEL	P58707 anthopleura
35	5	12.2	4	1	BIOA_CITFR	P01868 homo sapien
36	5	12.2	5	1	BIOB_CITFR	P13071 citrobacter
37	5	12.2	5	1	BIOB_CITFR	P12997 citrobacter
38	5	12.2	5	1	BIOB_CITFR	P82099 litorea rub
39	5	12.2	5	1	PRCT_PERAM	P01373 escherichia
40	5	12.2	5	1	TRM3_ECOLI	P13973 escherichia
41	5	12.2	6	1	CIP1_MYTED	P13737 mytilus edu
42	5	12.2	6	1	CIP2_MYTED	P13736 mytilus edu
43	5	12.2	6	1	FARP_MONEX	P41966 monelia ex
44	5	12.2	6	1	TRPI_PSEPU	P36414 pseudomonas
45	5	12.2	7	1	CHOX_ALCSP	P16101 alcaligenes

## ALIGNMENTS

RESULT 1  
WMW2\_ACHFU STANDARD; PRT; 7 AA.  
AC P35920;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE Wamide-2.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
CC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica.";  
RL FEBS Lett. 323:104-108(1993).  
DR PIR; S33246; S33246.  
KW Neuropeptide; Amidation.  
FT MOD\_RES  
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 41.5%; Score 17; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 0; Gaps 0;

QY 5 WKK 7  
||:  
Db 1 WKQ 3

RESULT 2  
WMW3\_ACHFU STANDARD; PRT; 7 AA.  
AC P35921;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE Wamide-3.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
CC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica.";  
RL FEBS Lett. 323:104-108(1993).  
DR PIR; S33244; S33244.  
KW Neuropeptide; Amidation.

FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;  
Query Match 41.5%; Score 17; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 WKX 7  
1 WKX 3

RESULT 3  
BPP7\_BOTIN STANDARD; PRT; 5 AA.

AC P30425;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide 55,2 (5A) (Angiotensin-converting enzyme inhibitor)  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=9031557; PubMed=2386615;  
RA Cima A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom."  
RL J. Protein Chem. 9:221-227(1990).  
CC - FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
CC PIR: G37196; G37196.  
DR KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 5 AA; 628 MW; 776DC37326B00000 CRC64;

Query Match 39.0%; Score 16; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KW 5  
1 WKX 3

RESULT 4  
WMA1\_ACHFU STANDARD; PRT; 7 AA.  
AC P35919;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE Wamide-1.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidae; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RA MEDLINE=93265912; PubMed=8495720;  
RX Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wamide-1", -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica."  
RL FEBS Lett. 323:104-108(1993).  
CC - FUNCTION: Exhibits modulatory effects on the peripheral nervous

CC system, inhibits activity on a central neuron.  
DR PIR: S33245; S33245.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;  
Query Match 34.1%; Score 14; DB 1; Length 7;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 WKX 7  
1 WKX 3

RESULT 5  
UF01\_MOUSE STANDARD; PRT; 5 AA.

AC P38639;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009987; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins using preparative two-dimensional gel electrophoresis."  
RL Electrophoresis 15:735-745(1994).  
CC - MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.6, its MW is: 19 kDa.  
CC NON\_TER 5  
FT MOD\_RES 5  
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 31.7%; Score 13; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KW 5  
1 WKX 5

RESULT 6  
TY51\_LITRU STANDARD; PRT; 7 AA.  
AC P82065;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Trypophyllin 5.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinbörner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog Litoria rubella". The skin peptide profile as a probe for the study of evolutionary trends of amphibians."  
RL Aust. J. Chem. 49:955-963(1996).  
CC - FUNCTION: May act as a neuromodulator or neurotransmitter.  
CC - SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=965; METHOD=FPAB.  
 KW Amphibian defense peptide; Amidation; Neuropeptide;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD RES 7 7 AMIDATION.  
 FT MOD RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 29.3%; Score 12; DB 1; Length 7;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 RMKW 5  
 DB 1 QIPW 4

## RESULT 7

OCPS OCTMI STANDARD; PRT; 4 AA.  
 ID OCPS OCTMI STANDARD; PRT; 4 AA.  
 AC P58643; 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cardioactive peptides Ocp-3/Ocp-4.  
 OS Octopus minor (Octopus).  
 CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Necoleoidea;  
 CC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
 OC NCBI\_TaxID=89766;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
 RC TISSUE=Brain;  
 RX MEDLINE=20336815; PubMed=10876044;  
 RA Iwakoshi E., Hisada M., Minakata H.;  
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
 RT Octopus minor.";  
 RL Peptides 21:623-630 (2000).  
 CC -1- FUNCTION: Cardioactive; has both positive chronotropic and  
 CC inotropic effects on the heart. Ocp-4 is a 1000 time less  
 CC active than Ocp-3.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: OCP-4 has D-Ser instead of L-Ser.  
 CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.  
 KW Hormone; D-amino acid.  
 FT MOD RES 2 2 D-SERINE (IN OCP-4).  
 FT MOD RES 4 4 463 MW; 6AB35B810000000 CRC64;  
 SQ SEQUENCE 4 AA; 463 MW; 6AB35B810000000 CRC64;

Query Match 26.8%; Score 11; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5  
 DB 3 W 3

## RESULT 8

E101\_LITRU STANDARD; PRT; 6 AA.  
 ID E101\_LITRU STANDARD; PRT; 6 AA.  
 AC P82056; 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Electrin 1.  
 OS Litoria rubella (Desert tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Hylidae;  
 CC Pelodyadinae; Litoria.  
 OC NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowler J.H., Tyler M.J., Wallace J.C.;

RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645 (1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD RES 6 6 AMIDATION.  
 FT MOD RES 6 6 AMIDATION.  
 SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 26.8%; Score 11; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5  
 DB 5 W 5

## RESULT 9

LOK1 LOCM1 STANDARD; PRT; 6 AA.  
 ID LOK1 LOCM1 STANDARD; PRT; 6 AA.  
 AC P41431; 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Locustastakinin I.  
 OS Locusta migratoria (Migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OC NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=92262851; PubMed=1585017;  
 RA Schoof L., Holman G.M., Proost P., van Damme J., Hayes T.K.,  
 RA de Looz A.;  
 RT "Locustastakinin, a novel myotropic peptide from Locusta migratoria,  
 RT isolation, primary structure and synthesis.";  
 RL Regul. Pept. 37:49-57 (1992).  
 CC -1- FUNCTION: Myotropic peptide. May be important in the stimulation  
 CC of ion transport and inhibition of diuretic activity in Malpighian  
 CC tubules.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC PIR; A61068; A61068.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 6 6 AMIDATION.  
 FT MOD RES 6 6 AMIDATION.  
 SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

Query Match 26.8%; Score 11; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5  
 DB 5 W 5

## RESULT 10

BRHP CONTIM STANDARD; PRT; 7 AA.  
 ID BRHP CONTIM STANDARD; PRT; 7 AA.  
 AC P58603; 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bromheptapeptide Im.  
 OS Conus imperialis (Imperial cone).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 CC Apogastropoda; Caenogastropoda; Sorbocochlea; Hypogastropoda;  
 CC Neogastropoda; Conoidea; Conidae; Conus.  
 OC NCBI\_TaxID=35631;  
 RN [1]

## RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

RC TISSUE=Venom; PubMed=9030520;  
 RX MEDLINE=91814108; J. Nielsen D.B., Guayas J.,  
 RA Craig A.G., Jimenez E.C., Dykert J.,  
 RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,  
 RA McIntosh J.M.;  
 RT "A novel post-translational modification involving bromination of  
 RT tryptophan. Identification of the residue, 1-6-bromotryptophan, in  
 RT peptides from *Conus imperialis* and *Conus radiatus* venom.";  
 RL J. Biol. Chem. 272:4689-4694(1997).  
 CC -1- FUNCTION: Does not elicit gross behavioral symptoms when injected  
 CC centrally or peripherally in mice.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MW=853.19; METHOD=LSIMS.  
 DR PIR, A58512, A58512;  
 KW Bromination; Amidation; Pyrrolidone carboxylic acid.  
 FT DISULFID 2 7  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 6 6 BROMINATION.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;

Query Match 26.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5  
 DB 6 W 6

RESULT 11  
 TPEY PACDA STANDARD; PRT; 7 AA.  
 ID TPEY PACDA STANDARD; PRT; 7 AA.  
 AC P83455;

DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tryptophyltin-1 (Pdt-1).  
 OS Pachymedusa daemnicolor (Giant Mexican leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Phyllomedusinae; Pachymedusa.  
 NC NCBI\_Taxid=75988;  
 RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
 RP PRO-7.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., Orr D.F., Shaw C.;

RT "Pachymedusa daemnicolor tryptophyltin-1 (Pdt-1): structural  
 RT characterization, pharmacological activity and cloning of precursor  
 RT cDNA.";  
 RL Submitted (SEP-2002) to Swiss-Proct.  
 CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
 CC smooth muscle.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.

CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.  
 KM Amphibian defense peptide; Amidation; Hydroxylation.  
 FT MOD\_RES 3 3  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 26.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5  
 DB 5 W 5

RESULT 12  
 VP19 HSV1K STANDARD; PRT; 6 AA.  
 ID VP19 HSV1K STANDARD; PRT; 6 AA.  
 AC P23210;

DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Capsid assembly and DNA maturation protein (Virion protein U138)  
 DE (Capsid protein VP19C) (Fragment).  
 GN U138.

OS Herpes simplex virus (type 1 / strain XOS).  
 OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 NC NCBI\_Taxid=10306;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91101287; PubMed=1846198;  
 RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,  
 RA Silverstein S., Wagner E.K.;  
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the  
 RT expression of U138, a true late gene involved in capsid assembly.";  
 RL J. Virol. 65:769-786(1991).  
 CC -1- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE  
 CC EMBEDDED. BINDS DNA.  
 CC -1- SIMILARITY: Belongs to the herpesviruses VP19C family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL, M57646; AAA45830.1; -;  
 KW Capsid assembly; Coat protein; DNA-binding.  
 FT NON\_TER 6  
 FT SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 24.4%; Score 10; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 MK 4  
 DB 1 MK 2

RESULT 13  
 FAR4\_HIRME STANDARD; PRT; 4 AA.  
 ID FAR4\_HIRME STANDARD; PRT; 4 AA.  
 AC P42563;

DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRamide-like neuropeptide YMR-amide.

OS Hirudo medicinalis (Medicinal leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Ahychrobellida; Hirudiniiformes; Hirudiniidae; Hirudo.  
 NC NCBI\_Taxid=6421;

RN [1]  
 RP SEQUENCE

RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl U., Karstons M.A., Calabrese R.L.;  
 RT "Identification of Rfamide neuropeptides in the medicinal leech.";  
 RL Peptides 12:897-908(1991).

CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.

KM Neuropeptide; Amidation.  
 FT MOD\_RES 4 4 AMIDATION.  
 SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 19.5%; Score 8; DB 1; Length 4;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MKW 5  
 DB 2 MRF 4

## RESULT 14

FMRP\_MACNI STANDARD; PRT; 4 AA.  
 ID FMRP\_MACNI  
 AC P01162;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE FMRPamide (peak C) (Cardioexcitatory neuropeptide).  
 OS Macrocallista nimbosa (Sun-ray clam).  
 OS Nereis virens (Sandworm).  
 OS Hirudo medicinalis (Medicinal leech), and  
 OS Helisoma trivolvis (Snail).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;  
 OC Veneroidea; Veneridae; Macrocallista.  
 OX NCBI\_TaxId=6594, 6353, 6421, 27815;  
 [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC SPECIES=N.nimbosa; TISSUE=Cerebral pedal, and visceral ganglion;  
 RX MEDLINE=77215956; PubMed=87582;  
 RA Price D.A., Greenberg M.J.;  
 RT "Structure of a molluscan cardioexcitatory neuropeptide."  
 RL Science 197;670-671(1977).  
 [2]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC SPECIES=M.nimbosa; TISSUE=Ganglion;  
 RX MEDLINE=78012038; PubMed=909675;  
 RA Price D.A., Greenberg M.J.;  
 RT "Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc."  
 RL Prep. Biochem. 7;261-281(1977).  
 [3]  
 RP SEQUENCE.  
 RC SPECIES=N.virens;  
 RX MEDLINE=90259866; PubMed=2342992;  
 RA Kraigher K.G., Price D.A.;  
 RT "Authentic FMRPamide is present in the polychaete Nereis virens."  
 RL Peptides 11;75-77(1990).  
 [4]  
 RP SEQUENCE.  
 RC SPECIES=H.medicalialis;  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of Rfamide neuropeptides in the medicinal leech."  
 RL Peptides 12;897-908(1991).  
 [5]  
 RP SEQUENCE.  
 RC SPECIES=H.trivolvis; TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRPamide-related peptides from the kidney of the snail, Helisoma trivolvis."  
 RL Peptides 15;31-36(1994).  
 CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological activities include augmentation, induction, and regularization of cardiac contraction.  
 CC -!- SIMILARITY: Belongs to the FMRP (FMRPamide related peptide) family.  
 DR PTR: A01426; ECKM.  
 DR PTR: A60418; A60418.  
 KM Neuropeptide; Amidation.  
 FT MOD\_RES 4  
 SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 19.5%; Score 8; DB 1; Length 4;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MKW 5  
 DB 2 MRF 4

## RESULT 15

FAR3\_HAECCO STANDARD; PRT; 7 AA.  
 ID FAR3\_HAECCO  
 AC P81298;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRPamide-like neuropeptide PF3 (KSAVMRF-amide).  
 OS Haemonchus contortus (Barber pole worm).  
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongyloida;  
 OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.  
 OX NCBI\_TaxId=6289;  
 [1]  
 RP SEQUENCE.  
 RC TISSUE=Neuron;  
 RX MEDLINE=99318264; PubMed=10391380;  
 RA Marks N.J., Sangster N.C., Maule A.G., Halton D.W., Thompson D.P.,  
 RA Geary T.G., Shaw C.;  
 RT "Structural characterisation and pharmacology of KHEVLRamide (Af2) and KSAVMRFamide (PF3/AF3) from Haemonchus contortus."  
 RL Mol. Biochem. Parasitol. 100;185-194(1999).  
 CC -!- FUNCTION: Active on neuromusculature.  
 CC -!- SIMILARITY: Belongs to the FMRP (FMRPamide related peptide) family.  
 CC Neuropeptide; Amidation.  
 KM MOD\_RES 7  
 SQ SEQUENCE 7 AA; 902 MW; 69D4068B5DC5350 CRC64;  
 [6]  
 QY 3 MKW 5  
 DB 5 MRF 7

Query Match 19.5%; Score 8; DB 1; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Search completed: August 11, 2004, 14:08:46  
 Job time : 14 secs

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ID Q8GL00 PRELIMINARY; PRT; 7 AA.  
 AC Q8GL00;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 GN PF-50 protein (Fragment).  
 OS Borrelia burgdorferi (Lyme disease spirochete).  
 OC Plasmid group cp32-13.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CA15;  
 RA Stevenson B., Miller J.C.;  
 RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
 RT phages: conservation amidst diversity."  
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY142106; AAN17857.1;  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 KM Plasmid.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

Query Match 39.0%; Score 16; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KW 5  
 DB 1 KW 2

RESULT 3  
 Q8KMS9 PRELIMINARY; PRT; 7 AA.  
 ID Q8KMS9;  
 AC Q8KMS9;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Putative transposase (Fragment).  
 GN TNA.  
 OS Enterobacter sp. CH2-4.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Enterobacter.  
 OX NCBI\_TaxID=14377;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CH2-4;  
 RX MEDLINE=21604134; PubMed=11763242;  
 RA Mirkin S.Z., Kholodil G.V., Gorlenko Z.M., Minakhina S.V.,  
 RA Mirakhin L.S., Kalyaeva E.S., Kopleva A.V., Petrova M.A.,  
 RA Yurleva O.V., Nikiforov V.G.;  
 RT "Mercury resistance transposons of Gram-negative environmental  
 RT bacteria and their classification."  
 RL Res. Microbiol. 152:811-822(2001).  
 DR EMBL; AJ302778; CAC85058.1;  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 966 MW; 737B1B1046DA9A0 CRC64;

Query Match 29.3%; Score 12; DB 2; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KW 5  
 DB 6 EW 7

RESULT 4  
 ID P92214 PRELIMINARY; PRT; 7 AA.  
 AC P92214;

DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Amblyopyrum muticum.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Amblyopyrum.  
 OX NCBI\_TaxID=4595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5572; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data."  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77756; CAB01346.1;  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KM Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRM 3  
 DB 5 RRL 7

RESULT 5  
 P92393 PRELIMINARY; PRT; 7 AA.  
 ID P92393;  
 AC P92393;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Hordeum vulgare (Barley).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H3139; TISSUE=leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data."  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77756; CAB01370.1;  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KM Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRM 3  
 DB 5 RRL 7

RESULT 6



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P92403 PRELIMINARY; PRT; 7 AA.
ID P92403;
AC P92403;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
DE 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Lophopyrum elongatum (Tall wheatgrass) (Aegopyrum elongatum).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Thinopyrum.
OX NCBI_TaxID=4588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6692; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77743; CAB01307.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRM 3
|:|:
DB 5 RRL 7

RESULT 7
P92427 PRELIMINARY; PRT; 7 AA.
ID P92427;
AC P92427;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
DE 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Ribosomal protein (Fragment).
GN RPS11.
OS Peridictyon sanctum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Peridictyon.
OX NCBI_TaxID=37683;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5575; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77749; CAB01325.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRM 3
|:|:
DB 5 RRL 7

```

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RESULT 8
P92430 PRELIMINARY; PRT; 7 AA.
ID P92430;
AC P92430;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
DE 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6668; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77758; CAB01352.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRM 3
|:|:
DB 5 RRL 7

```

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RESULT 9
P92221 PRELIMINARY; PRT; 7 AA.
ID P92221;
AC P92221;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
DE 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Bromus inermis (Smooth brome grass).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Bromaceae; Bromus.
OX NCBI_TaxID=15371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OSA414; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01355.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 RRM 3  
||:  
Db 5 RRL 7

## RESULT 10

PRELIMINARY; PRT; 7 AA.  
ID P92425  
AC P92425;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
GN Ribosomal protein 11 (Fragment).  
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Pseudoroegneria.  
OX NCBI\_TaxID=4604;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H9082; TISSUE=leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.,  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77744; CAB01310.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KM Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRM 3  
||:  
Db 5 RRL 7

## RESULT 11

PRELIMINARY; PRT; 7 AA.  
ID P92381  
AC P92381;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
GN Ribosomal protein 11 (Fragment).  
OS Hordeum brachyantherum.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=52712;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.,  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77741; CAB01361.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KM Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;

Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRM 3  
||:  
Db 5 RRL 7

## RESULT 12

PRELIMINARY; PRT; 7 AA.  
ID P92387  
AC P92387;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
GN Ribosomal protein 11 (Fragment).  
OS Henrardia persica.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Henrardia.  
OX NCBI\_TaxID=3678;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5556; TISSUE=leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.,  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77748; CAB01322.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KM Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRM 3  
||:  
Db 5 RRL 7

## RESULT 13

PRELIMINARY; PRT; 7 AA.  
ID P92210  
AC P92210;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
GN Agropyron cristatum (Crested wheatgrass).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Agropyron.  
OX NCBI\_TaxID=4593;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H4349; TISSUE=leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.,  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77771; CAB01391.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KM Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 1

SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRM 3  
||:  
Db 5 RRL 7

DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRM 3  
||:  
Db 5 RRL 7

Search completed: August 11, 2004, 14:09:32  
Job time : 36 secs

RESULT 14  
P92440 PRELIMINARY; PRT; 7 AA.  
AC P92440;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Thincopyrum bessarabicum.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Thincopyrum.  
OX NCBI\_TaxID=4601;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6725; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; 277767; CAB01355.1;-  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRM 3  
||:  
Db 5 RRL 7

RESULT 15  
P92218 PRELIMINARY; PRT; 7 AA.  
AC P92218;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Australopyrum retrofractum.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Australopyrum.  
OX NCBI\_TaxID=4597;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6723; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; 277767; CAB01379.1;-

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:02:18 ; Search time 50 Seconds  
(without alignments)  
39.557 Million cell updates/sec

Title: US-09-854-204-2  
Perfect score: 41  
Sequence: 1 RRMKWK 7  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 92273

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003s:\*  
7: Geneseqp2004s:\*  
8: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	7	AAV83540	AAV83540 Peptide f
2	41	100.0	7	ADL14766	ADL14766 Carrier m
3	41	100.0	7	ADL14762	ADL14762 Drosophil
4	41	100.0	7	ABG15504	ABG15504 Fruit fly
5	41	100.0	7	AAE17558	AAE17558 Fluoresce
6	41	100.0	7	AAW48627	AAW48627 Anti-infl
7	41	100.0	7	AAW48620	AAW48620 Anti-infl
8	41	100.0	7	ABP60478	ABP60478 NLS pepit
9	41	100.0	7	ABP60478	ABP60478 Anti-infl
10	41	100.0	7	ADA61903	ADA61903 NFKB esse
11	41	100.0	7	ADA61896	ADA61896 NFKB esse
12	41	100.0	7	ADC22330	ADC22330 Nuclear l
13	38	92.7	7	AAV83544	AAV83544 Peptide f
14	38	92.7	7	AAV83543	AAV83543 Peptide f
15	38	92.7	7	ADL14767	ADL14767 Drosophil
16	38	92.7	7	ADL14766	ADL14766 Peptide f
17	36	87.8	7	AAV83546	AAV83546 Peptide f
18	36	87.8	7	AAV83539	AAV83539 Peptide f
19	36	87.8	7	ADL14769	ADL14769 Drosophil
20	35	85.4	7	AAV83547	AAV83547 Peptide f
21	35	85.4	7	ADL14770	ADL14770 Drosophil
22	34	82.9	7	AAV83545	AAV83545 Peptide f
23	34	82.9	7	ADL14768	ADL14768 Drosophil
24	33	80.5	7	AAV83549	AAV83549 Peptide f
25	33	80.5	7	ADL14772	ADL14772 Drosophil

26	29	70.7	7	AAV83550	AAV83550 Peptide f
27	29	70.7	7	ADL14773	ADL14773 Drosophil
28	28	68.3	7	AAV83548	AAV83548 Peptide f
29	28	68.3	7	ADL14771	ADL14771 Drosophil
30	27	65.9	7	AAW48057	AAW48057 AB14 sub
31	26	63.4	4	ABR00881	ABR00881 Bioactive
32	26	63.4	5	ABR00892	ABR00892 Bioactive
33	26	63.4	6	AAW65537	AAW65537 Lipopept
34	25.5	62.2	7	AAV83551	AAV83551 Peptide f
35	25.5	62.2	7	AAV83553	AAV83553 Peptide f
36	25.5	62.2	7	ADL14774	ADL14774 Drosophil
37	25.5	62.2	7	ADL14775	ADL14775 Drosophil
38	25	61.0	7	AAI21287	AAI21287 Human sem
39	24	58.5	7	AAW38781	AAW38781 Delivery
40	24	58.5	7	AAV83552	AAV83552 Peptide f
41	24	58.5	7	AAV83554	AAV83554 Peptide f
42	23	56.1	4	AAW43242	AAW43242 Peptide f
43	23	56.1	5	AAE21734	AAE21734 BSMR effe
44	23	56.1	6	AAV83552	AAV83552 Antimicro
45	23	56.1	2	AAV83553	AAV83553 Antimicro

## ALIGNMENTS

RESULT 1	AAV83540	standard; peptide; 7 AA.
ID	AAV83540	
XX	AAV83540	
AC		
XX	29-AUG-2000	(first entry)
DT		
XX		
DE	Peptide fragment of membrane transport vector penetratin.	
XX		
KW	Penetratin; translocation; membrane; drug delivery; therapy; treatment; conjugate; vector.	
KM		
XX		
OS	Synthetic.	
XX		
PN	WO200029427-A2.	
XX		
PD	25-MAY-2000.	
XX		
PE	11-NOV-1999; 99WO-GB003750.	
XX		
PR	13-NOV-1998; 98GB-00025000.	
PR	13-NOV-1998; 98GB-00025001.	
PR	04-FEB-1999; 99GB-00002522.	
PR	04-FEB-1999; 99GB-00002525.	
PR	22-JUN-1999; 99GB-00014578.	
XX		
PA	(CYCL-) CYCLACEL LTD.	
XX		
PI	Fischer MF, Zhelev N;	
XX		
DR	WPI, 2000-387734/33.	
XX		
PT	New membrane translocation peptide carrier group for delivering	
PT	therapeutic agents into target cells comprises specified sequence of	
PT	amino acids.	
PS	Claim 5; Page 26; 59pp; English.	
XX		
CC	Penetratin is a membrane translocation polypeptide and as such, active	
CC	peptide fragments of penetratin can be used to translocate conjugated	
CC	molecules across the cell membrane e.g. drugs. 13 chemical entities are	
CC	described for use in the method such as paclitaxel-	
CC	2'-succinimidopropionyl-Cbetar-RRMKWK-NH <sub>2</sub> , and podophylotoxin-4-	
CC	succinimidopropionyl-Cbetar-RRMKWK-NH <sub>2</sub> . The method has applications as	
CC	a drug delivery system for treatment and therapy. The resulting	
CC	conjugated molecules exhibit high immunogenicity, solubility and	
CC	clearance. The penetratin peptide fragment may be truncated and or have	

CC amino acid substitutions. See GENESSEQ records AAY83520-Y83581

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
| | | | |  
DB 1 RRMKKKK 7

RESULT 2

ID ADE14786 standard; peptide; 7 AA.

AC ADE14786;

DT 29-JAN-2004 (first entry)

DE Carrier moiety SegID26 related to improved drug delivery.

KM drug delivery system; carrier group; homeobox peptide; drug metabolism;  
KM drug biodistribution; drug excretion; drug half life; drug solubility;  
KM drug side-effect; drug resistance; penatrin; antennapedia homeodomain;  
KM fruit fly; mutant; mutein.

OS Synthetic.

OS Drosophila melanogaster.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Optionally C-terminal H"

FT Modified-site 7 /note= "N-terminal amide"

PN WO200001417-A1.

PD 13-JAN-2000.

PF 22-JUN-1999; 99WO-GB001957.

PR 03-JUL-1998; 98GB-00014527.

PA (CYCL-) CYCLACEL LTD.

PI Fischer PM, Wang S;

DR WPI; 2000-160729/14.

PT Delivery systems with improved delivery into target cells, half-life, solubility in biological fluids, enhanced metabolism, biodistribution and excretion, and minimal toxic side-effects.

Claim 33; SEQ ID NO 26; 114bp; English.

CC This invention relates to novel drug delivery systems comprising a drug group linked to a carrier group comprising a homeobox peptide, its fragment or derivative. The invention may provide a method of improved delivery into target cells with enhanced metabolism, biodistribution and excretion of a drug. The drug may be therapeutically active in both intact and dissociated states. The invention may improve half-life of a drug in human or animal bodies, improve solubility in biological fluids, minimize known toxic or non-desirable side-effects, enhance onset of action of a desired therapeutic effect, provide alternative routes for administration of drug and decrease incidence of drug resistance. The present sequence is the amino acid sequence of a carrier peptide derived from penatrin, a peptide derived from the antennapedia homeodomain of Drosophila melanogaster. The drug and carrier moieties associated with this sequence in the exemplification of the invention are featured.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
| | | | |  
DB 1 RRMKKKK 7

RESULT 3

ID ADE14762 standard; peptide; 7 AA.

AC ADE14762;

DT 29-JAN-2004 (first entry)

DE Drosophila melanogaster homeodomain truncated penatrin peptide SegID2.

KM drug delivery system; carrier group; homeobox peptide; drug metabolism;  
KM drug biodistribution; drug excretion; drug half life; drug solubility;  
KM drug side-effect; drug resistance; penatrin; antennapedia homeodomain;  
KM fruit fly.

OS Drosophila melanogaster.

PN WO200001417-A1.

PD 13-JAN-2000.

PF 22-JUN-1999; 99WO-GB001957.

PR 03-JUL-1998; 98GB-00014527.

PA (CYCL-) CYCLACEL LTD.

PI Fischer PM, Wang S;

DR WPI; 2000-160729/14.

PT Delivery systems with improved delivery into target cells, half-life, solubility in biological fluids, enhanced metabolism, biodistribution and excretion, and minimal toxic side-effects.

Claim 9; SEQ ID NO 2; 114bp; English.

CC This invention relates to novel drug delivery systems comprising a drug group linked to a carrier group comprising a homeobox peptide, its fragment or derivative. The invention may provide a method of improved delivery into target cells with enhanced metabolism, biodistribution and excretion of a drug. The drug may be therapeutically active in both intact and dissociated states. The invention may improve half-life of a drug in human or animal bodies, improve solubility in biological fluids, minimize known toxic or non-desirable side-effects, enhance onset of action of a desired therapeutic effect, provide alternative routes for administration of drug and decrease incidence of drug resistance. The present sequence is the amino acid sequence of a truncated form of penatrin, a peptide derived from the antennapedia homeodomain of Drosophila melanogaster, which is related to the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
| | | | |  
DB 1 RRMKKKK 7

RESULT 4

ABG75504  
ID ABG75504 standard; peptide; 7 AA.  
AC ABG75504;  
XX  
XX  
DT 14-APR-2003 (first entry)  
XX  
XX  
DE Fruit fly Antp-HD truncated membrane translocation sequence #2.  
XX  
XX Translocation; delivery vehicle; agent-membrane translocation sequence;  
XX MTS; membrane translocation sequence; plasma membrane; red blood cell;  
XX immunisation; antigen; intracellular delivery; therapeutic; HIV-1;  
XX trans-activating protein; Tat; Antennapedia homeodomain protein; Antp-HD;  
XX VP22 protein; HSV-VP22; signal-sequence-based peptide; Transportin;  
XX Amphiphilic model peptide; Fruit fly.  
XX  
XX Drosophila sp.  
XX  
XX US2002151004-A1.  
XX  
XX 17-OCT-2002.  
XX  
XX 16-FEB-2001; 2001US-00785802.  
XX  
XX 24-JUL-2000; 2000WO-G8002848.  
XX 09-AUG-2000; 2000WO-G8003056.  
XX 22-DEC-2000; 2000US-00748063.  
XX 22-DEC-2000; 2000US-00748789.  
XX  
XX (CRAI/) CRAIG R.  
XX  
XX Craig R;  
XX  
XX MPI; 2002-260593/32.  
XX  
XX Preparing a red blood cell vehicle suitable for delivering an agent to a  
XX target site in a vertebrate due to loading the red blood cell with an  
XX agent-membrane translocation sequence.  
XX  
XX  
XX PS Disclosure; Page 8; 43pp; English.  
XX  
XX The invention discloses a method for preparing a delivery vehicle for  
XX delivering an agent to a target site in a vertebrate. The method  
XX comprises loading a cell with an agent-membrane translocation sequence  
XX (MTS) conjugate, which contains a membrane translocation sequence  
XX enabling the agent to cross the plasma membrane of a cell. Also disclosed  
XX is a pharmaceutical composition comprising a red blood cell for delivery  
XX of an agent to a vertebrate, the red blood cell comprising the novel  
XX agent-MTS conjugate and a method of immunisation of an animal with an  
XX antigen. The method is useful for preparing delivery vehicles,  
XX particularly a red blood cell, for the intracellular delivery of a  
XX therapeutic agent to a target site. The method is particularly useful for  
XX enabling an agent to cross the plasma membrane of a target cell, and for  
XX selectively releasing the agent-MTS conjugate at a target site to  
XX facilitate the uptake of the agent by the cells at the target site. The  
XX preferred MTS sequences are from HIV-1 trans-activating protein (Tat),  
XX Drosophila Antennapedia homeodomain protein (Antp-HD), Herpes Simplex-1  
XX virus VP22 protein (HSV-VP22), a signal-sequence-based peptide and a  
XX Transportin and Amphiphilic model peptide. The sequence presented is the  
XX active truncated Fruit fly MTS, #2  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred.No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRMKMKK 7  
| | | | |  
| | | | |  
Db 1 RRMKMKK 7

RESULT 5

AAE17558  
ID AAE17558 standard; peptide; 7 AA.  
AC AAE17558;  
XX  
XX  
DT 22-APR-2002 (first entry)  
XX  
XX  
DE Fluorescent timer fusion proteins constructing NLS peptide #16.  
XX  
XX Fluorescent timer protein; protein movement; translocation; trafficking;  
XX promoter activity; gene expression; transgenic plant; gene modification;  
XX protein age; nuclear localisation signal; NLS.  
XX  
XX Unidentified.  
XX  
XX WO200196373-A2.  
XX  
XX 20-DEC-2001.  
XX  
XX 13-JUN-2001; 2001WO-US019097.  
XX  
XX 14-JUN-2000; 2000US-0211607P.  
XX  
XX (CLON-) CLONTECH LAB INC.  
XX  
XX Fradkov AF, Tersikh A;  
XX  
XX MPI; 2002-154595/20.  
XX  
XX  
XX PT New fluorescent timer proteins comprising an emission spectrum that  
XX changes over time from a first wavelength to a second wavelength, useful  
XX for monitoring intracellular protein movement, translocation, trafficking  
XX or stability.  
XX  
XX  
XX PS Disclosure; Page 18; 89pp; English.  
XX  
XX The invention relates to a fluorescent timer protein having an emission  
XX spectrum that changes over time after synthesis from a first wavelength  
XX to a second wavelength. The fluorescent timer proteins are useful in  
XX monitoring the activity of a promoter, determining the age of a protein,  
XX identifying an agent that modulates the activity of a promoter and in  
XX enriching a population of cells comprising a fluorescent timer protein.  
XX The fluorescent timer proteins are also useful for assessing gene  
XX expression during development of a multicellular organism or during  
XX cellular differentiation, in response to a drug or other inducer of  
XX promoter activity, as a reporter to serve as a read-out of promoter  
XX activity, monitoring intracellular protein movement or translocation,  
XX protein trafficking, or protein stability, to investigate temporal  
XX aspects of the activity of a regulatory element, for determining cell  
XX fate during development and organ remodelling, in spatial and temporal  
XX visualisation of newly synthesised proteins and accumulated proteins, and  
XX in distinguishing between newly formed and pre-existing structures, e.g.  
XX membrane junctions and extracellular matrix components. The fluorescent  
XX timer proteins may further be used to investigate structures where photobleaching  
XX techniques are employed, as detectable labels, as selectable markers, as  
XX biosensors in prokaryotic and eukaryotic cells, in process cleavage  
XX assays, and as second messenger detectors. The nucleic acids can be used  
XX to generate transgenic, non-human plants or animals or site-specific gene  
XX modifications in cell lines. The present sequence is nuclear localisation  
XX signal (NLS) peptide used for constructing fluorescent timer proteins  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred.No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRMKMKK 7  
| | | | |  
| | | | |  
Db 1 RRMKMKK 7

RESULT 6

AA48627	standard; peptide; 7 AA.
AA48627	
AA48627	
20-MAR-2002	(first entry)
Anti-inflammatory peptide SEQ ID NO 130.	
Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;	
antiinflammatory; antiarthritic; osteoprotic; antibacterial; virucide;	
immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;	
antiallergic; membrane translocation domain; NEMO binding domain; eczema;	
cyclokin; NFKappB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;	
rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;	
autoimmune disorder; multiple sclerosis; transplant rejection;	
osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;	
ataxia telangiectasia; allergy; anaphylaxis; arthritis.	
Synthetic.	
WO200183554-A2.	
08-NOV-2001.	
02-MAY-2001; 2001WO-US014346.	
02-MAY-2000; 2000US-0201261P.	
22-NOV-2000; 2000US-00643260.	
(PRAE-) PRAECS PHARM INC.	
(UYIA ) UNIV YALE.	
May MJ, Ghosh S, Findeis MA, Phillips K;	
WPI; 2002-121889/16.	
Novel antiinflammatory compound comprising membrane translocation domain	
fused to NEMO binding sequence, useful for blocking nuclear factor kappaB	
activation, and for treating asthma, lung inflammation, psoriasis.	
Claim 11; Page 62; 88pp; English.	
The invention relates to an antiinflammatory compound (especially	
AA48628-AA48645), comprising a membrane translocation domain (AA48620-	
AA48627 or AA48646-AA48651) which comprises from 6-15 amino acid	
residues, fused to a NEMO binding sequence (AA48525-AA48619). The	
antiinflammatory compounds have antiasthmatic, cyostatic, antipsoriatic,	
antiinflammatory, antiarthritic, osteoprotic, antibacterial,	
immunosuppressive, dermatological, neuroprotective, nootropic,	
antiatherosclerotic, virucide and antiallergic activity. The compounds	
act as selective inhibitors of cytokine-mediated NFKappab activation by	
blocking interaction of Ikappab kinase beta (IKKbeta) at the NEMO binding	
domain that results in inhibition of IKKbeta kinase activation and	
subsequent decreased phosphorylation of kappaB. The compounds are useful	
for treating inflammatory disorders, e.g. asthma, lung inflammation or	
cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory	
bowel disease, sepsis, vasculitis, dermatitis, autoimmune diseases such as	
lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;	
transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;	
viral infections; and ataxia telangiectasia. The compounds are also	
useful for treating pro-inflammatory responses such as allergies,	
urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,	
sunburn, aging and arthritis	
Sequence 7 AA;	
Query Match	100.0%; Score 41; DB 5; Length 7;
Best Local Similarity	100.0%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

QY 1 RRMKWK 7

Db 1 FRMKWK 7

RESULT 7  
AA048620 ID AA048620 standard; peptide; 7 AA.

XX AA048620:  
XX  
XX 20-MAR-2002 (first entry)  
XX  
XX Anti-inflammatory peptide SEQ ID NO 123.  
XX  
XX Antihistaminic; antiallergic; cytoprotic; antipsoriatic; nootropic;  
XX antirheumatic; antiarthritic; osteoprotic; antibacterial; vitaminid;  
XX immunosuppressive; dermatological; neuroprotective; antialtherosclerotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anapylaxis; arthritis.  
XX  
XX Synthetic.  
XX  
XX WO200183554-A2.  
XX  
XX 08-NOV-2001.  
XX  
XX 02-MAY-2001; 2001WO-US014346.  
XX  
XX 02-MAY-2000; 2000US-0201261P.  
XX 22-AUG-2000; 2000US-0064326C.  
XX  
XX (PRAE) PRAECIS PHARM INC.  
XX (UYVA) UNIV YALE.  
XX  
XX May MJ, Ghosh S, Findeis MA, Phillips K;  
XX WPI; 2002-121889/16.  
XX  
XX Novel antiinflammatory compound comprising membrane translocation domain  
XX fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
XX activation, and for treating asthma, lung inflammation, psoriasis.  
XX  
XX Claim 11; Page 62; 88pp; English.  
XX  
XX The invention relates to an antiinflammatory compound (especially  
XX AA048620-AA048645), comprising a membrane translocation domain (AA048620-  
XX AA048627 or AA048646-AA048651) which comprises from 6-15 amino acid  
XX residues, fused to a NEMO binding sequence (AA048625-AA048619). The  
XX antiinflammatory compounds have antiseptic, cytosolic, antipsoriatic,  
XX antirheumatic, antiarthritic, osteoprotic, antibacterial,  
XX immunosuppressive, dermatological, neuroprotective, nootropic,  
XX antialtherosclerotic, vitaminid and antiallergic activity. The compounds  
XX act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
XX blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
XX domain that results in inhibition of IKKbeta kinase activation and  
XX subsequent decreased phosphorylation of IkappaB. The compounds are useful  
XX for treating inflammatory disorders, e.g. asthma, lung inflammation or  
XX cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
XX bowel disease, sepsis, vasculitis, bursts; autoimmune diseases such as  
XX lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
XX transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
XX viral infections; and ataxia telangiectasia. The compounds are also  
XX useful for treating pro-inflammatory responses such as allergies,  
XX urticaria, anapylaxis, drug or food sensitivity, eczema, dermatitis,  
XX sunburn, aging and arthritis  
XX  
XX Sequence 7 AA;

Query Match	100.0%;	Score 41;	DB 5;	Length 7
Best Local Similarity	100.0%;	Pred. No. 1.4e+06;		



Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
| | | | |  
1 RRMKMKK 7

RESULT 8  
ID ABP60478 standard; peptide; 7 AA.  
XX

AC ABP60478;

XX 10-MAY-2003 (first entry)

DE NLS peptide SEQ ID NO 17.

XX Protease; detection; drug screening; caspase; apoptosis; infection;

KW nuclear localisation signal; NLS.

XX Unidentified.

XX WO2003012393-A2.

XX 13-FEB-2003.

XX 30-JUL-2002; 2002WO-US024119.

XX 31-JUL-2001; 2001US-0309112P.

XX (CLON-) CLONTECH LAB INC.

XX Haugwitz M;

XX WPI; 2003-248202/24.

PT Detecting the presence of active protease in a cell for use in protease  
PT activity detection and drug screening applications, by using a protease  
PT detection fusion protein.

XX Disclosure; Page 10; 43pp; English.

XX The invention relates to a cell comprising a protease detection fusion  
CC protein containing first and second subcellular localisation domains (D1,  
CC D2) separated by a cleavage domain (CD) recognised by the protease,  
CC (where D1 is dominant over D2 and a label domain is present between CD  
CC and D2). The fusion protein is maintained for a period of time sufficient  
CC for CD to be cleaved by protease if present in the cell and subcellular  
CC localisation of label domain is detected. The method is useful for  
CC determining whether a cell contains an active protease. The method finds  
CC applications, including monitoring activity of a protease in a cell,  
CC monitoring the effect of an agent on the activity of a protease, e.g. for  
CC drug screening applications to identify agents that modulate the activity  
CC of a particular protease and studying the effect of a factor on  
CC expression of the protease-encoding gene. Detecting protease activity of  
CC interest in a cell is useful for determining the particular state of the  
CC cell associated with the particular protease, e.g. certain active  
CC caspases indicate that a cell is undergoing an apoptotic event. Protease  
CC detection applications can be used in diagnostic applications, including  
CC diagnosis of bacterial and/or viral pathogenic infection. The present  
CC sequence is that of a nuclear localisation signal (NLS) containing  
CC peptide disclosed in illustrations of the invention

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
| | | | |  
1 RRMKMKK 7

RESULT 9  
ID ABP6972 standard; peptide; 7 AA.  
XX

AC ABP6972;

XX 17-JUN-2003 (first entry)

DE Anti-inflammatory polypeptide SEQ ID NO:11.

XX Anti-inflammatory; inflammatory disorder; polybasic; antiallergic;  
KW cytoskeletal; tuberculostatic; nephrotoxic; antineoplastic; antiallergic;  
KW dermatological; immunosuppressive; antiallergic; antiparasitic; asthma;  
KW gynaecological; ophthalmological; chromolytic; protein therapy;  
KW lung inflammation; cancer; chronic granulomatous disease; tuberculosis;  
KW leprosy; sarcoidosis; silicosis; nephritis; rheumatoid arthritis;  
KW amyloidosis; ankylosing spondylitis; chronic bronchitis; scleroderma;  
KW lupus; appendicitis; psoriasis; pelvic inflammatory disease; allergy;  
KW orbital inflammatory disease; thrombotic disease.

XX Synthetic.

XX WO2003020213-A2.

XX 13-MAR-2003.

XX 27-AUG-2002; 2002WO-US027421.

XX 30-AUG-2001; 2001US-0316328P.

XX (PRAE-) PRAECIS PHARM INC.

XX Lazarus D; Hannig G;

XX WPI; 2003-354457/33.

PT New polybasic peptide useful for treating inflammatory disorders, such as  
PT asthma, lung inflammation, cancer, chronic granulomatous diseases,  
PT nephritis, amyloidosis, rheumatoid arthritis, scleroderma or allergies.

XX Claim 34; Page 23; 35pp; English.

XX The present invention describes an anti-inflammatory compound comprising  
CC a polybasic peptide (I). (I) comprises the structure: B1-X1-X2-X3-B2-X4-  
CC X5-B3, or B1-X1-X2-B2-B3-X3-X4-B4, where B1, B2, B3 and B4 = basic amino  
CC acid residues; and X1, X2, X3, X4 and X5 = alpha-helix promoting amino  
CC acid residues. Also described: (1) methods of treating an inflammatory  
CC disorder in a subject; and (2) a method for modulating the secretion of  
CC pro-inflammatory cytokines in a cell. (I) has cytostatic,  
CC antiinflammatory, antiallergic, tuberculostatic, nephrotoxic,  
CC antineoplastic, antiparasitic, dermatological, immunosuppressive,  
CC antiallergic, antiparasitic, gynaecological, ophthalmological and  
CC thrombolytic activities, and can be used in protein therapy. The  
CC composition and method are useful in treating inflammatory disorders,  
CC such as asthma, lung inflammation, cancer, chronic granulomatous diseases  
CC (e.g. tuberculosis, leprosy, sarcoidosis or silicosis), nephritis,  
CC amyloidosis, rheumatoid arthritis, ankylosing spondylitis, chronic  
CC bronchitis, scleroderma, lupus, appendicitis, psoriasis, pelvic  
CC inflammatory disease, orbital inflammatory disease, thrombotic disease  
CC and allergies. The present sequence represents a specifically claimed  
CC anti-inflammatory polybasic peptide from the present invention

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
| | | | |  
1 RRMKMKK 7

RESULT 10  
ADA61903  
ID ADA61903 standard; peptide; 7 AA.  
XX  
AC ADA61903;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE NFkB essential modulator (NEMO) binding peptide #103.  
XX  
NM NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KM antiinflammatory; antiaesthetic; antipsoriatic; antirheumatic;  
KM antirheumatic; osteopathic; antibacterial; immunosuppressive;  
KM dermatological; neuroprotective; cytostatic; nocitropic; virucide;  
KM gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KM psoriasis; rheumatoid arthritis; osteoarthritis;  
KM inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KM systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KM Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KM necrosis factor kappa B essential modulator.  
XX  
OS Unidentified.  
XX  
PN US2003054999-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 02-MAY-2001; 2001US-00847946.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PA (MAYM/) MAY M J.  
PA (GHOS/) GHOSH S.  
PA (FIND/) FINDERIS M A.  
PA (PHIL/) PHILLIPS K.  
PA (HANN/) HANNIG G.  
XX  
PI May MJ, Ghosh S, Funderis MA, Phillips K, Hannig G;  
XX  
DR WPI; 2003-596541/56.  
XX  
PT New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.  
XX  
PS Claim 11; Page 24; 37pp; English.  
XX  
CC The invention describes an anti-inflammatory compound comprising (1). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC ADA61896;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE NFkB essential modulator (NEMO) binding peptide #96.  
XX  
NM NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KM antiinflammatory; antiaesthetic; antipsoriatic; antirheumatic;  
KM antirheumatic; osteopathic; antibacterial; immunosuppressive;  
KM dermatological; neuroprotective; cytostatic; nocitropic; virucide;  
KM gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KM psoriasis; rheumatoid arthritis; osteoarthritis;  
KM inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KM systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KM Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KM necrosis factor kappa B essential modulator.  
XX  
OS Unidentified.  
XX  
PN US2003054999-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 02-MAY-2001; 2001US-00847946.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PA (MAYM/) MAY M J.  
PA (GHOS/) GHOSH S.  
PA (FIND/) FINDERIS M A.  
PA (PHIL/) PHILLIPS K.  
PA (HANN/) HANNIG G.  
XX  
PI May MJ, Ghosh S, Funderis MA, Phillips K, Hannig G;  
XX  
DR WPI; 2003-596541/56.  
XX  
PT New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.  
XX  
PS Claim 11; Page 24; 37pp; English.  
XX  
CC The invention describes an anti-inflammatory compound comprising (1). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
ADC22330  
ID ADC22330 standard; peptide; 7 AA.  
XX  
AC ADC22330;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Nuclear localization signal motif amino acid sequence SEQ ID NO:179.

XX recombinant fusion protein; fusion protein; binding; detection;  
 KW localisation domain; binding domain;  
 KM subcellular compartment localisation.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003012068-A2.  
 XX  
 PD 13-FEB-2003.  
 XX  
 PF 01-AUG-2002; 2002WO-US024572.  
 XX  
 PR 01-AUG-2001; 2001US-0309395P.  
 PR 13-DEC-2001; 2001US-0341589P.  
 XX  
 PA (CELL-) CELLONICS INC.  
 XX  
 PI Bright G, Premkumar DR, Chen Y;  
 DR WPI; 2003-248174/24.  
 XX  
 XX New recombinant fusion protein comprising detection and first  
 PT localization domains and a binding domain for the molecule of interest.  
 PT useful for detecting binding of a molecule of interest.  
 PT  
 PS Claim 20; SEQ ID NO 179; 101p; English.  
 XX  
 CC The present invention describes a recombinant fusion protein (I) for  
 CC detecting binding of a molecule of interest. (I) comprises: (a) a  
 CC detection domain; (b) a first localisation domain; and (c) a binding  
 CC domain for the molecule of interest. The detection domain, the first  
 CC localisation domain and the binding domain for the molecule of interest  
 CC constituting the recombinant fusion protein for detecting binding of a  
 CC molecule of interest are operably linked. The binding domain for the  
 CC molecule of interest is separated from the first localisation domain by 0  
 CC -20 amino acid residues. The first localisation domain and the binding  
 CC domain for the molecule of interest both do not occur in a single non-  
 CC recombinant protein with the same spacing as in the recombinant fusion  
 CC protein for detecting binding of a molecule of interest. Also described:  
 CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;  
 CC (2) a recombinant expression vector comprising the nucleic acid control;  
 CC sequences operably linked to the recombinant nucleic acid molecule; (3) a  
 CC genetically engineered host cell transfected with the recombinant  
 CC expression vector; (4) a kit for detecting binding of the molecule of  
 CC interest; and (5) a method for identifying compounds that alter the  
 CC binding of the molecule of interest. The recombinant fusion protein is  
 CC useful for detecting binding of a molecule of interest. The recombinant  
 CC fusion protein eliminates the need to construct two or more chimeric  
 CC proteins and enables the monitoring of biochemical events in live, intact  
 CC or fixed cells. The present sequence is used in the exemplification of  
 CC the present invention.  
 CC  
 SQ Sequence 7 AA;  
 XX  
 XX  
 Query Match 100.0%; Score 41; DB 7; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKWKX 7  
 | | | | | | |  
 DB 1 RRMKWKX 7  
 RESULT 13  
 ID AAY83544 standard; peptide; 7 AA.  
 XX  
 AC AAY83544;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Peptide fragment of membrane transport vector penetratin.

XX Penetratin; translocation; membrane; drug delivery; therapy; treatment;  
 KW conjugate; vector.  
 KM  
 XX Synthetic.  
 OS  
 XX WO200029427-A2.  
 XX  
 PN 25-MAY-2000.  
 XX  
 PD 11-NOV-1999; 99WO-GB003750.  
 XX  
 PF 13-NOV-1998; 98GB-00025000.  
 PR 13-NOV-1998; 98GB-00025001.  
 PR 04-FEB-1999; 99GB-00002522.  
 PR 04-FEB-1999; 99GB-00002525.  
 PR 22-JUN-1999; 99GB-00014578.  
 XX  
 PA (CYCL-) CYCLACEL LTD.  
 XX  
 PI Fischer MP, Zhelev N;  
 DR WPI; 2000-387734/33.  
 XX  
 XX New membrane translocation peptide carrier group for delivering  
 PT therapeutic agents into target cells comprises specified sequence of  
 PT amino acids.  
 PT  
 PS Claim 7; Page 26; 59pp; English.  
 XX  
 CC Penetratin is a membrane translocation polypeptide and as such, active  
 CC peptide fragments of penetratin can be used to translocate conjugated  
 CC molecules across the cell membrane e.g. drugs, 13 chemical entities are  
 CC described for use in the method such as paclitaxel-  
 CC 2-succinimidopropionyl-Cbeta-RMKK-NH<sub>2</sub>, and podophylotoxin-4-  
 CC succinimidopropionyl-Cbeta-RMKK-NH<sub>2</sub>. The method has applications as  
 CC a drug delivery system for treatment and therapy. The resulting  
 CC conjugated molecules exhibit high immunogenicity, solubility and  
 CC clearance. The penetratin peptide fragment may be truncated and or have  
 CC amino acid substitutions. See GENESEQ records AAY83520-Y83581  
 CC  
 SQ Sequence 7 AA;  
 XX  
 XX  
 Query Match 92.7%; Score 38; DB 3; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKWKX 7  
 | | | | | | |  
 DB 1 RRMKWKX 7  
 RESULT 14  
 ID AAY83543 standard; peptide; 7 AA.  
 XX  
 AC AAY83543;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Peptide fragment of membrane transport vector penetratin.  
 KW Penetratin; translocation; membrane; drug delivery; therapy; treatment;  
 KM conjugate; vector.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200029427-A2.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 11-NOV-1999; 99WO-GB003750.  
 XX

PR 13-NOV-1998; 98GB-00025000.  
 PR 13-NOV-1998; 98GB-00025001.  
 PR 04-FEB-1999; 99GB-00002522.  
 PR 04-FEB-1999; 99GB-00002525.  
 PR 22-JUN-1999; 99GB-00014578.

XX (CYCL-) CYCLACEL LTD.

XX Fischer MP, Zhelev N;

XX WPI; 2000-387734/33.

XX New membrane translocation peptide carrier group for delivering

PT therapeutic agents into target cells comprises specified sequence of

XX amino acids.

XX Claim 5; Page 26; 59pp; English.

XX Penetration is a membrane translocation polypeptide and as such, active

CC peptide fragments of penetratin can be used to translocate conjugated

CC molecules across the cell membrane e.g. drugs. 13 chemical entities are

CC described for use in the method such as paclitaxel.

CC 2/succinimidopropionyl-L-betaa-RRMKWK-NH 2, and podophyllotoxin-4-

CC succinimidopropionyl-L-betaa-RRMKWK-NH 2. The method has applications as

CC a drug delivery system for treatment and therapy. The resulting

CC conjugated molecules exhibit high immunogenicity, solubility and

CC clearance. The penetratin peptide fragment may be truncated and or have

CC amino acid substitutions. See GENSEQ records AAY83520-Y83581

XX Sequence 7 AA;

XX Query Match 92.7%; Score 38; DB 3; Length 7;

XX Best Local Similarity 85.7%; Pred. No. 1.4e+06;

XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

PT solubility in biological fluids, enhanced metabolism, biodistribution and

PT excretion, and minimal toxic side-effects.

XX Disclosure; SEQ ID NO 7; 114pp; English.

XX This invention relates to novel drug delivery systems comprising a drug

CC group linked to a carrier group comprising a homeobox peptide, its

CC fragment or derivative. The invention may provide a method of improved

CC delivery into target cells with enhanced metabolism, biodistribution and

CC excretion of a drug. The drug may be therapeutically active in both

CC intact and dissociated states. The invention may improve half-life of a

CC drug in human or animal bodies, improve solubility in biological fluids,

CC minimise known toxic or non-desirable side-effects, enhance onset of

CC action of a desired therapeutic effect, provide alternative routes for

CC administration of drug and decrease incidence of drug resistance. The

CC present sequence is the amino acid sequence of a truncated and mutated

CC form of penetratin, a peptide derived from the antennapedia homeodomain of

CC Drosophila melanogaster, which is related to the invention.

XX Sequence 7 AA;

XX Query Match 92.7%; Score 38; DB 3; Length 7;

XX Best Local Similarity 85.7%; Pred. No. 1.4e+06;

XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

XX : |||||

XX 1 RRMKWK 7

Search completed: August 11, 2004, 14:08:22  
 Job time : 51 secs

PT Delivery systems with improved delivery into target cells, half-life,

Page 1

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1 RESULT 1
2 US-09-854-204-2
3 Sequence 2, Application US/09854204
4 Patent No. US20020098236A1
5 GENERAL INFORMATION:
6 APPLICANT: Fischer, Peter Martin
7 APPLICANT: Zhelev, Nikolai
8 TITLE OF INVENTION: Transport Vectors
9 FILE REFERENCE: CCI-010
10 CURRENT APPLICATION NUMBER: US/09/854,204
11 CURRENT FILING DATE: 2001-05-11
12 PRIOR APPLICATION NUMBER: 09/438,460
13 PRIOR FILING DATE: 1999-11-12
14 PRIOR APPLICATION NUMBER: GB 9825000.4
15 PRIOR FILING DATE: 1998-11-13
16 PRIOR APPLICATION NUMBER: GB 9825001.2
17 PRIOR FILING DATE: 1998-11-13
18 PRIOR APPLICATION NUMBER: GB 9902525.6
19 PRIOR FILING DATE: 1999-02-04
20 PRIOR APPLICATION NUMBER: GB 9902522.3
21 PRIOR FILING DATE: 1999-02-04
22 PRIOR APPLICATION NUMBER: GB 9914578.1
23 PRIOR FILING DATE: 1999-06-22
24 PRIOR APPLICATION NUMBER: PCT/GB99/03750
25 PRIOR FILING DATE: 1999-11-11
26 NUMBER OF SEQ ID NOS: 66
27 SOFTWARE: PatentIn Ver. 2.1
28 SEQ ID NO 2
29 LENGTH: 7
30 TYPE: PRT
31 ORGANISM: Artificial Sequence
32 FEATURE:
33 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
34 OTHER INFORMATION: sequence
35 NAME/KEY: MOD_RES
36 LOCATION: (7)
37 OTHER INFORMATION: AMIDATION; the carboxy terminal lysine residue may
38 OTHER INFORMATION: have its carboxyl group converted into an

```

OTHER INFORMATION: carboxamide group.  
US-09-854-204-2

Query Match 100.0%; Score 41; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWK 7  
Db 1 RRMKWK 7

## RESULT 2

US-09-785-802A-6  
Sequence 6, Application US/09785802A  
Patent No. US20020151004A1  
GENERAL INFORMATION:  
APPLICANT: Craig, Roger  
TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME  
FILE REFERENCE: 11067/3035  
CURRENT APPLICATION NUMBER: US/09/785,802A  
PRIOR FILING DATE: 2001-02-16  
PRIOR APPLICATION NUMBER: US 09/748,06  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/748,789  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-785-802A-6

Query Match 100.0%; Score 41; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWK 7  
Db 1 RRMKWK 7

## RESULT 3

US-09-847-946A-123  
Sequence 123, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamnig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 123  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:membrane  
US-09-847-946A-123

Query Match 100.0%; Score 41; DB 10; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWK 7  
Db 1 RRMKWK 7

## RESULT 4

US-09-847-946A-130  
Sequence 130, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamnig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 130  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:membrane  
US-09-847-946A-130

Query Match 100.0%; Score 41; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWK 7  
Db 1 RRMKWK 7

## RESULT 5

US-10-144-549-4  
Sequence 4, Application US/10144549  
Publication No. US20030211590A1  
GENERAL INFORMATION:  
APPLICANT: Genesuticte Biopharm, Inc.  
APPLICANT: Hwu, Paul L.  
TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR  
FILE REFERENCE: MBHB 02-340  
CURRENT APPLICATION NUMBER: US/10/144,549  
CURRENT FILING DATE: 2002-05-13  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-10-144-549-4

Query Match 100.0%; Score 41; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWK 7  
Db 1 RRMKWK 7

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RESULT 6
US-10-229-915-11
; Sequence 11, Application US/10229915
; Publication No. US20030083262A1
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Douglas
; APPLICANT: Hamms, Gerhard
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: FPI-127
; CURRENT APPLICATION NUMBER: US/10/229,915
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/316,328
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-inflammatory compound
US-10-229-915-11

Query Match          100.0%; Score 41; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7
DB 1 RRMKKK 7

RESULT 7
US-10-211-088-179
; Sequence 179, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins And Assays For Molecular B
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 179
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Nuclear localization signal
US-10-211-088-179

Query Match          100.0%; Score 41; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7
DB 1 RRMKKK 7

RESULT 8
US-10-210-660-2
; Sequence 2, Application US/10210660
; Publication No. US20030119735A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Fischer, M. Peter
; APPLICANT: Wang, Shudong
; TITLE OF INVENTION: Delivery System
; FILE REFERENCE: CCI-009
; CURRENT APPLICATION NUMBER: US/10/210,660
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US/09/346,847
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: GB 9814527
; PRIOR FILING DATE: 1998-07-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-210-660-2

Query Match          100.0%; Score 41; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7
DB 1 RRMKKK 7

RESULT 9
US-10-210-660-26
; Sequence 26, Application US/10210660
; Publication No. US20030119735A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, M. Peter
; APPLICANT: Wang, Shudong
; TITLE OF INVENTION: Delivery System
; FILE REFERENCE: CCI-009
; CURRENT APPLICATION NUMBER: US/10/210,660
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US/09/346,847
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: GB 9814527
; PRIOR FILING DATE: 1998-07-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)_
; OTHER INFORMATION: AMIDATION
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-210-660-26

Query Match          100.0%; Score 41; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7
DB 1 RRMKKK 7

RESULT 10
US-10-315-920-22
; Sequence 22, Application US/10315920
```

Publication No. US20030175809A1  
GENERAL INFORMATION:  
APPLICANT: Trakov, Arcady Fedorovich  
APPLICANT: Terexikh, Alexey  
TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS  
TITLE OF INVENTION: FOR THEIR USE  
FILE REFERENCE: CLON-077CIP  
CURRENT APPLICATION NUMBER: US/10/315,920  
CURRENT FILING DATE: 2002-12-09  
PRIOR APPLICATION NUMBER: 60/211,607  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: PCT/US01/19097  
PRIOR FILING DATE: 2001-06-13  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: nuclear localization signal  
US-10-315-920-22

Query Match 100.0%; Score 41; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
DB 1 RRMKWK 7

RESULT 11  
US-09-854-204-9  
Sequence 9, Application US/09854204  
Patent No. US20020098236A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, Peter Martin  
APPLICANT: Zhelev, Nikola  
TITLE OF INVENTION: Transport Vectors  
FILE REFERENCE: CCI-010  
CURRENT APPLICATION NUMBER: US/09/854,204  
CURRENT FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 09/438,460  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: GB 9825000.4  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9825001.2  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9902525.6  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9902522.3  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9914578.1  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: PCT/GB99/03750  
PRIOR FILING DATE: 1999-11-11  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-854-204-9

Query Match 92.7%; Score 38; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7

DB 1 RRMKWK 7

RESULT 12  
US-09-854-204-10  
Sequence 10, Application US/09854204  
Patent No. US20020098236A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, Peter Martin  
APPLICANT: Zhelev, Nikola  
TITLE OF INVENTION: Transport Vectors  
FILE REFERENCE: CCI-010  
CURRENT APPLICATION NUMBER: US/09/854,204  
CURRENT FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 09/438,460  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: GB 9825000.4  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9825001.2  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9902525.6  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9902522.3  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9914578.1  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: PCT/GB99/03750  
PRIOR FILING DATE: 1999-11-11  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-854-204-10

Query Match 92.7%; Score 38; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
DB 1 RRMKWK 7

RESULT 13  
US-10-210-660-6  
Sequence 6, Application US/10210660  
Publication No. US20030119735A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
APPLICANT: Wang, Shudong  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/10/210,660  
CURRENT FILING DATE: 2002-07-31  
PRIOR APPLICATION NUMBER: US/09/346,847  
PRIOR FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-210-660-6

Query Match 92.7%; Score 38; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7



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Page 5

US-10-210-660-6

Query Match 92.7%; Score 38; DB 14; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWKX 7  
DB 1 KRMKWKX 7

RESULT 14

US-10-210-660-7  
Sequence 7; Application US/10210660  
Publication No. US20030119735A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
APPLICANT: Wang, Shudong  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/10/210,660  
CURRENT FILING DATE: 2002-07-31  
PRIOR APPLICATION NUMBER: US/09/346,847  
PRIOR FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-210-660-7

Query Match 92.7%; Score 38; DB 14; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWKX 7  
DB 1 KRMKWKX 7

RESULT 15

US-09-854-204-12  
Sequence 12; Application US/09854204  
Patent No. US20020098236A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, Peter Martin  
APPLICANT: Zhelev, Nikolai  
TITLE OF INVENTION: Transport Vectors  
FILE REFERENCE: CCI-010  
CURRENT APPLICATION NUMBER: US/09/854,204  
CURRENT FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 09/438,460  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: GB 9825000.4  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9825001.2  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9902525.6  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9902522.3  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9914578.1  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: PCT/GB99/03750  
PRIOR FILING DATE: 1999-11-11  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 12  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-854-204-12

Query Match 87.8%; Score 36; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKWKX 7  
DB 1 RRMKWKX 7

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